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                                                                                                                                                                                                                                                                                                                           The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or a retention deficient disorder, a schizoaffective disorder, a bipolar or a unipolar affective disorder. The DPIs are used in proteomics. The proteomic approach of using DPIs for screening, diagnosis or prognosis of system (CNS) tissue from a living patient under normal circumstances. The present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                           Preparation for diagnosing or treating bipolar affected disorder (BAD) unipolar depression, or for screening for modulators, comprises a BAD-associated protein isoform.
CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder; unipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizophrenia, neuroleptic, diagnostic, neuropsychiatric disorder, neurological disorder; neuropathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizophrenia-associated isoform peptide #198.
                                                                                                                                                                                        (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                              Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                         Claim 8; Page 34; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU15313 standard; peptide; 7 AA
                                                                                                                                       24-FEB-2000; 2000GB-00004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                                                  23-FEB-2001; 2001WO-GB000791.
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Best Local Similarity 42.5%,
                                                                                                                                                                                                                                    WPI; 2001-582081/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 FTLKISR 7
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                                                                    WO200163294-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
                                               Homo sapiens.
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                                                                                           30-AUG-2001
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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFs) and SCH Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, contemporate active abundance of at least 1 chosen feature correlates with the presence or absence of SCH, and (1) screening or diagnosis of SCH and the relative abundance of SCH, and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIs and related molecules (e.g. of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of sch in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of neuropsychiatric disorders. AAUISII4-AAUIS762 represent the maino acid sequences of schizophrenia-associated corrections in the mathod of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAUI5762 represent the amino acid sequences isoforms used in the method of the invention
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                                                                                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                      Rohlff C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 32; 160pp; English.
                                                               23-FEB-2001; 2001WO-GB000783
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                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-502868/55
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Best Local Similarity
Matches 3; Conserv
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YTFELSR 7
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                                                                                                                          24-FEB-2000;
28-DEC-2000;
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30-AUG-2001
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us-09-712-819c-6.closed.rag

RESULT 11 AAU28602

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New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                  Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, Bipolar Affective Disorder, BAD, Depression-Associated feature, DF, Depression-Associated protein isoform, DFI, Cerebro-spinal fluid,
                                                                                                                                                                                                                                                                                       Schizophrenia-Associated Protein Isoform (SPI) peptide #198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.6%; Score 20; DB 4; Length 7; 42.9%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rohlff C, Terrett JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Depression-Associated Protein isoform DPI-208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 32; 148pp; English.
                                                                                                                                                      AAU24969 standard; peptide; 7 AA.
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28-DEC-2000; 2000US-00750395.
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1 YTFELSR
1 FTLKISR
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                                                                                                                                                                                                                                             18-DEC-2001
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Best Local S
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                                                                                                             RESULT 12
AAU24969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU2887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), maniac-depressive illnesses, attention deficit disorders, schizoaffective disorders, and unipolar affective disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, depression associated protein isoform; tryptic digest peptide; DPI; cerebrospinal fluid, CSF; BAD; bipolar affective disorder; neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
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                                                                                 Score 20; DB 4; Length 7; Pred. No. 1.4e+06; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maniac-depressive illness; schizoaffective disorder
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treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rohlff C,
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                                                                                                                                                                                                                                                                                                                                    AAU28602 standard; peptide; 7 AA.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                   60.68;
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Best Local Similarity 42.9
Matches 3; Conservative
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                                                                                   Query Match
Best Local Similarity
Matches 3; Conserv
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1 YTFELSR
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                                        Sequence 7 AA;
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Gaps

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comprises analyzing body fluid by 2-dimensional electrophoresis for
features correlated with VD.
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Claim 6; Page 31; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy

Sequence 7 AA;

Gaps . 0 Match 60.6%; Score 20; DB 4; Length 7; Local Similarity 42.9%; Pred. No. 1.4e+06; es 3; Conservative 3; Mismatches 1; Indels Query Match

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RESULT 9 ABB56283

ABB56283 standard; peptide; 7 AA

15-FEB-2002 (first entry)

Vascular dementia-associated protein isoform (VPI) 483.

VD; VD-associated protein isoform; VPI; screening; Vascular Dementia; VD; VD-associate diagnosis; prognosis; gene therapy

Homo sapiens

20-SEP-2001

WO200169261-A2

14-MAR-2001; 2001WO-GB001106.

15-MAR-2000; 2000GB-00006285. 24-NOV-2000; 2000GB-00028734. 28-NOV-2000; 2000US-00724391.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Rohlff C; Herath HMAC, Parekh RB,

WPI; 2001-557937/62.

Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.

Claim 6; Page 40; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance

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correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the severening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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Pred. No. 1.4e+06;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                             60.68;
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.3%,
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RESULT 10 ABB55981

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ABB55981 standard; peptide; 7 AA.

ABB55981;

15-FEB-2002

Vascular dementia-associated protein isoform (VPI) 181.

Vascular Dementia, VD, VD-associated protein isoform; VPI; screening; diagnosis; prognosis; gene therapy.

Homo sapiens.

WO200169261-A2.

20-SEP-2001

14-MAR-2001; 2001WO-GB001106.

15-MAR-2000; 2000GB-00006285. 24-NOV-2000; 2000GB-00028734. 28-NOV-2000; 2000US-00724391.

(OXFO-) OXFORD GLYCOSCIENCES UK LID.

Rohlff Herath HMAC,

ΰ

WPI; 2001-557937/62.

for nsetul Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.

Claim 6; Page 33; 151pp; English.

The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of erebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) from the subject one of 223 VD-associated protein isoforms (VPIS) ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the

Wright SD;

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Peptides AAR81847-54 are tryptic peptide fragments from human afamin (AAR81845) novel member of the human serum protein family. The fragments were used to design primers and probes (AAT00786-98) for the cloning of the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to have similar properties to human albumin, alpha-foetoprotein and vitamin D binding protein due to homology with these proteins. The gene encodes a mature protein of 66576 daltons without post-translational processing (ca. 87000 daltons with post-translational processing). The protein was isolated from human plasma by a conventional chromatographic methods. The protein can be used to ameliorate ischaemia-reperfusion injury, rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma substances released after inflammation, etc
                                                                                                                                                                    Human afamin or a variant and poly:nucleotide(s) encoding it - a human serum protein with activities in common with other members of this family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, rheumatoid arthritis, RA, diagnosis, RPI, RADF, detection, rheumatoid arthritis diagnostic feature, BRPI, synovial fluid, rheumatoid arthritis diagnostic protein isoform, screening, expression reference protein isoform, prognosis.
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                                                                                                                         Wurfel MM,
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                                                                                                                                                                                                                                                 Example 3; Page 45; 97pp; English.
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                31-MAR-1995; 95WG-US004075.
                                            94US-00222619
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                                                                                                                        Lichenstein HS, Lyons DE,
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                                                                         (AMGE-) AMGEN INC.
(UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                       WPI; 1995-358634/46.
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FTFEYSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7 AA;
                                             31-MAR-1994;
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A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally comparises in the electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen comparing the abundance of each chosen feature whose relative abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as CC RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as protocols. AAY41844 to AAY41800 represent RPI peptides, AAY42101 to AAX425066 to AAX25066 to AAX25066 to AAX25066 to AAX25068 represent degenerate probes for RPIS, which are all the exemplification of the present invention
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  human rheumatoid arthritis by two-dimensional
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42.9%; Pred. No. 1.4e+06;
iive 3; Mismatches 1; Indels
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                                                                                                         Disclosure; Page 18; 157pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB55870 standard; peptide; 7 AA.
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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Best Local Similarity 42.9
Matches 3; Conservative
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1 YTFELSR 7
                                      electrophoresis
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ABB55870
ID ABB5:
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AC ABB5:
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AAB30076;

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A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally symbolic synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen comparing the abundance of each chosen feature whose relative abundance of that chosen feature in the configuration of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence of the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-chagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as protocols. Any41844 to Any42100 represent expression reference protein isoform poptides and AAZ55066 to AAZ25068 represent degenerate probes for RPIS, which are all used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                               Diagnosis of human rheumatoid arthritis by two-dimensional
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Best Local Similarity 83.3%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                        (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 21; 157pp; English
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                                                                                                                                                                                    Parekh RB, Patel TP,
                                                                                                                                                                                                                                   WPI; 1999-571871/48.
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                                                                                                                                                                                                                                                                                                           electrophoresis.
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                                             15-MAR-1999;
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 23-SEP-1999.
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AAR81848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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                                                                                                                                                                                                        Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atheroselerosis.
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                                                                                                                                                        Scaffold protein SCA S4 peptide SEQ ID NO: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 15, 68pp; English.
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                 AAB30076 standard; peptide; 7 AA
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                                                                                                          09-FEB-2001 (first entry)
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Homo sapiens WO9947925-A2

AAY42013;

à g 01-APR-1999; 01-APR-1999; 12-OCT-2000.

Synthetic.

84 derivative #12, beta strand of scaffold protein structure.

à g

AAY40738 standard; peptide; 7 AA.

AAY40738;

FTLSIS

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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                             69.7%; Score 23; DB 2; Length 7; 83.3%; Pred. No. 1.4e+06; tive 0; Mismatches 1; Indels
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Best Local Similarity 83.5
Las 5; Conservative
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                                                                                                                                                                                                                                                                                            Sequence 7 AA;
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ID AAB
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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structure the scaffold is constructed of two beta sheets, with the structure of the scaffold is constructed of two beta sheets, with the structure of the scaffold other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to target the complex to tumour cells. Therefore the scaffold protein may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a protein which binds to a tumour antigen. This will target the complex to specific cells. It may also be used to change to changues for specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in constant to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New scaffold protein, useful for stabilizing antigens used as vaccines.
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                                                                                                                                                                                                                                                                                                                                                                                                   Scaffold protein; beta strand; beta sheet; stabilize antigen; tumour; chemotherapeutic agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 6; 105pp; English.
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5; Conservative
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RESULT 3
AAY40738
ID AAY4
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RESULT 4

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Gaps

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Query Match 69.7%; Score 23; DB 3; Length 7; Best Local Similarity 83.3%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 1; Indels

1 FTLKIS 6

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June 1, 2004, 10:40:31; Search time 45.6667 Seconds (without alignments) 43.310 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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92273 1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-712-819C-6 33 1 FTLKISR 7 Title: Perfect score: Scoring table: Searched: Sequence:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 29Jan04:* Database :

geneseqp1980s:*
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geneseqp2000s:*
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geneseqp2003as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES		
Result No.	Score	* Query Match 1	Length	DB	п	Description	ion
	23	69.7	7	į ~	AAY40736		S4 deriva
7	23	69.7	7	m	AAB30074	Aab30074	- 6
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4	22	66.7	7	ო	AAB30076	Aab30076	Tr.
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7	20	9.09	7	N	AAY41889	Ø	Rheumatoi
80	20	ö	7	4	ABB55870,	Abb55870	Vascular
6	20	9.09	7	4	ABB56283	Abb56283	Vascular
10	20	ö	7	4	ABB55981	Abb55981	Vascular
	20	0	7	4	AAU28602	Aau28602	DPI trypt
12	20	9.09	7	4	AAU24969	Aau24969	Schizophr
	20	0	7	4	AAU26249	Aau26249	Depressio
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15	50	9.09	7	4	ABB52190	Abb52190	Human API
16	20	0	7	4	ABB52355	Abb52355	Human API
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	20	O	7	S	ABG78730	Abg78730	Multiple
	20	0	7	9	ABP58010	Abp58010	Prostate
20	20	9.09	7	9	ABP57255	Abb57255	
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ALIGNMENTS

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent. S4 derivative #10, beta strand of scaffold protein structure. AAY40736 standard, peptide; 7 AA. (first entry) 01-DEC-1999 EP947582-A1 Synthetic. AAY40736; RESULT 1
AAY40736
ID AAY4
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XX AAY4
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98EP-00870065. 31-MAR-1998; 06-OCT-1999

98EP-00870065. (INNO-) INNOGENETICS NV. 31-MAR-1998;

Hufton S, Hoogenboom H, Sablon E;

Desmet J,

New scaffold protein, useful for stabilizing antigens used as vaccines. Disclosure; Page 6; 105pp; English. WPI; 1999-542958/46.

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands C form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold is used to stabilize antigens

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EMBL; U75692; AAC49682.1; -.
GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
GO; GO:0016829; F:1yase activity; IEA.
          Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                               COCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Collagenase-3 (Fragment).
MMP13.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                    SEQUENCE FROM N.A.
MEDLINE=97351561; PubMed=9207843;
Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
"Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in Suspension cultures of tomato (Lycopersicon esculentum).";
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063480;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
TR4-NS orphan receptor (Fragment).
TR4.
Rattus norvegicus (Rat).
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SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. OX NOBL_TaxID=10116; RN [1]
RP SEQUENCE FROM N.A.
RX WEDLINE=9619874; PubMed=8612486; RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M., RA Detera-Wadleigh S.D.; RT "Splice variants of rat TR4 orphan receptor: differential expression RT domain."; RE Endocrinology 137:1562-1571(1996). DR EMBL; US9125; AAB02827.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1 1 1
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64; Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps QV KI S DE 11 KI 2
DB 1 KI Search completed: June 1, 2004, 11:18:37
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Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY142106; AAN17857.1; -.

GO: GO:0046821; C:extrachromosomal DNA; IEA.
                                              Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-13.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
  24, Last annotation update)
                         PF-50 protein (Fragment).
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P9323
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Stevenson B., Miller J.C.;
Comparative analyses of Borrelia burgdorferi erp genes and their cp32
Prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142100; AAN17911.1;
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=93-0107;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
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Q8GL04;
Q8GL04;
Q8GL04;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Q1-JUN-2003 (TremBLrel. 24, Last annotation update)
PF-50 protein (Fragment).
PF-50.
Borrelia burgdorferi (Lyme disease spirochete).
Prasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI TaxID=139;
                                                                                                                                                                                       Plasmid group cp32-9.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
EMBL; AY142103; AAN17848.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PP-50 protein (Fragment).
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SEQUENCE 7 AA, 914 MW; 6337244330504310 CRC64;
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SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;
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(TrEMBLrel. 23, Last sequence update)
                                                                                                                                                           Borrelia burgdorferi (Lyme disease spirochete)
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                             STRAIN=N40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid.
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OBGLOO;
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Matches
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Q8GL00
ID Q8GL0
AC Q8GL0
DT 01-MA
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Q8GL04
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
(Clone XP6A11A) (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
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                                                                      Query Match 27.3%; Score 9; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P93233;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
(Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
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NON TER 7 7 7 7 SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;
NON_TER 1 1 1
SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;
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STRAIN=RF-1;
MEDLINE=99231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                Rattus sp.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801)
Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Gunn;
MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
EMBL; S38636; AAB19259.1; -.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.3%; Score 9; DB 11; Length 4; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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                                                                                                    008433;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nifk (Fragment).
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SEQUENCE 4 AA; 473 MW; 633732C42000000 CRC64;
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SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
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                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiology 145:743-753(1999).
EMBL; AF003700; AAC35193.1; -.
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                                                                                PRELIMINARY;
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SEQUENCE FROM N.A.
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Q8GL12
ID Q8GL12
                                                                                  Q08433
                         RESULT 7
Q08433
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SEQUENCE, ALWARO; TISSUB-Leaf;

XA Yamaguchi K., von Knoblauch K., Subramanian A.R.;

MEDLINE=20435797; PubMed=10874039;

XT "The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 37:28455-28465(2000).

C. !- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

C. !- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

C. !- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

C. !- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

C. !- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

C. !- FUNCTION: THIS PROTEIN W=10477.0; METHOD=ELECTROSPRAY.

C. !- MASS SPECTROMETRY: WW=10477.0; METHOD=ELECTROSPRAY.

C. !- MASS SPECTROMETRY: WW=10497; O; METHOD=ELECTROSPRAY.

C. !- MASS SPECTROMETRY: WW=10477.0; METHOD=ELECTROSPRAY.

C. !- MASS SPECTROMETRY: WH=10477.0; METHOD=ELECTROSPRAY.

C. !- MASS 
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Caryophylales, Amaranthaceae, Spinacia.
                                                                             STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.3%; Score 11; DB 8; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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PB2541;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2003 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 30S ribosomal protein S19 beta (Fragment).
Spinacia oleracea (Spinach).
                                                                                                                                                                                                                                     J. Biol. Chem. 255:11927-11941(1980).

EMBL, V00694; CAA24066.1; -.

GO, GO:0005739; C:mitochondrion; IEA.

Mitochondrion.

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SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;
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SEQÜENCE 6 AA; 732 MW; 63333735A411C000 CRC64;
                                                  SEQUENCE FROM N.A.
NCBI_TaxID=4932;
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SEQUENCE.
STRAIN=DSM 20451;
PubMed=12112860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
"High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095945;
01-FEB-1997 (TrEMBLrel, 02, Created)
01-FEB-1997 (TrEMBLrel, 02, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
Inside intron 5 (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
Mitochondrion.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P83530 PRELIMINARY; PRT; 7 AA.
P83530;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI_TAXID=1625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.4%; Score 12; DB 5; Length 7; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043704; AAO38592.1; -.
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
Bradshaw H., Graves T., Blair T., "The sequence of C. elegans cosmid W01B11."; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Waterston R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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NON_TER 7 7
SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;
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Q95945
ID Q9594
AC Q9594
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XE MEDLINE=20435798; PubMed=10874046;

XETAINE=20435798; PubMed=10874046;

Yamaguchi K., Subramanian A.R.;

Yamaguchi K., Subramanian A.R.;

XI The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

XI J. Biol. Chem. 275:28466-28482(2000).

XI J. Biol. Chem. 275:28482(2000).

XI J. Biol. Chem. 275:28
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea (Spinach).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
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0721C0;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein W01B11.6.
W01B11.6.
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SEQÜENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
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MEDLINE=99069613; PubMed=9851916;
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SEQUENCE FROM N.A.
STRAIN-Bristol N2;
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RESULT 3 Q7Z1C0

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June 1, 2004, 10:53:46 ; Search time 31.3333 Seconds (without alignments) 70.488 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_organelle:*
sp_phage:*
sp_plant:*
sp_vodent:*
sp_vortebrate:*
sp_unclassified:*
sp_rvirus:*
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SUMMARIES

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م م	•		14, Last sunctation update)	7 0)	Щ Н	ledc	ort							ific	ome		ĽĽY		님	SI >	AILY			ä		Ë.	Ribosomal protein; Chloroplast; rRNA-binding.		6321B415B05DB000 CRC64;	Score 13; DB 10;	Pred. No. 1e+06;	Mismatches
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TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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P81808;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatin 5.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TAXID=6759;
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Query Match

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RESULT 11 PSK_DAUCA ID PSK D

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TISSUE=Cerebral ganglion, and Thoracic ganglion;

MEDLINE=98121193; PubMed=9461295;

A Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

Thorpe A.;

"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";

Eur. J. Biochem. 250:727-734(1997).

L. -!- FUNCTION: May act as a neurotransmitter or neuromodulator.

-!- SIMILARITY: Belongs to the allatostatin family.

Mouropeptide; Amidation; Multigene family.

MOD RES

7 AA; 770 MW; 672879CDESDDB70 CRC64;
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Bur. J. Biochem. 250:727-734(1997).

-!- FUNCTION: May act as a neurotransmitter or neuromodulator.

-!- SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Multigene family.

SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
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MEDLINE=98121193; Pubmed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.,
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab)
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.
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Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
Daucus carota (Carrot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Daucinae;
                                                                                                                                                                                                                                   Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCÉLLULAR LOCATION: Secreted.
-!- PTM: Sulfation is important for activity and for the binding to putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINS.

STRAINS.

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STRAINS.

MEDLINE=20212743; Pubmed=10750705;

Hanai H., Matsubayashi Y., Kobayashi T.,

Kamada H., Sakagami Y.;

"A secreted peptide growth factor, phytosulfokine, acting as a stimulatory factor of carrot somatic embryo formation.";

Plant Cell Physiol. 41:27-32(2000).

-!- FUNCTION: In presence of 2,4-D, stimulates proliferation of the cells, but does not stimulate differentiation into the somatic
                                                                                                                                                                                                                                   ;
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 allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD RES 5 AMIDATION (POTENTIAL).
SEQÜENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
ALL2 CARMA

ID ALL2 CARMA

AC P818\(\text{05}\)5;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

Carcinustatin 2.

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                24.2%; Score 8; DB 1; Length 5; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 3 SULFATION.
5 AA; 687 MW; 76C1BB504B300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHYTOSULFOKINE-BETA SULFATION.
                                                                                                                                                                                                        Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                       1 FTL 3
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P58261;
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TISSUE=Coleoptile;
Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6.0, its MW is: 30.0 kDa.
Maize-2DPAGE; P80630; COLEOPTILE.
MaizeDB; 123956; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                  UC24 MAIZE STANDARD; PRT; 7 AA.
P80630;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
(Fragment).
Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.; "Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carcinustatin 14.
Carcinustatin 14.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1. PIR; A25269; A25269. Pheromone. Pheromone. 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.3%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; ative 0; Mismatches 1; Indels
                                                                                                                                       27.3%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indels
                                                                                    7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
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AL14 CARMA

ID AL14 CARMA

STANDARD; PRT; 5 AA.

AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
Carcinus maens (Common shore crab) (Green crab).
Carcinus maens (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacco C Eumalacostraca; Eucarida; Decapoda; Pleocyemata; OX NCBI TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion; RX MEDLINE=98121193; PubMed=9461295;
RA Thorpe A.;
RA Thorpe A.;
RT "Isolation and identification of multiple neurope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Cerebral ganglion, and Thoracic ganglion; MEDLINE=98121193; PubMed=9461295;
                                                                                                                                                             Local Similarity 66.7
es 2; Conservative
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2; Conserva
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Best Local S
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UC24 MAIZE
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01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidase from Alcaligenes sp.";
J. Biochem. 88:197-203(1980).
-!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2)
PIR; A15398; A15398.
Oxidoreductase.
NON TER
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7
SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;
J. Biol. Chem. 263:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
PIR; A30812; A30812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81006769; PubMed-6997283;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
"Identification and properties of the prosthetic group of choline
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Alcaligenaceae; Alcaligenes.
NCBI_TaxID=512;
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-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.

-!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                      27.3%; Score 9; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05; Live 0; Mismatches 0; Indels
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                                                                                                                                     72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA; 839 MW; 7415B1E457644AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Choline oxidase (EC 1.1.3.17) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AA.
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MEDLINE=87005252; PubMed=3093276;
                                                                                                                                   7 AA; 790 MW;
                                                                                                                                                                                                                 Local Similarity 100.
Les 2; Conservative
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                                                                                                               Pheromone.
SEQUENCE
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Best Local S:
Matches 2
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CCF1 ENTFA STANDARD; PRT; 7 AA.

P20104;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone CCF10.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI TaxID=1351;
     TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
-!- MISCELLANFOUS: On the 2D-gel the determined pl of this unknown protein is: 6.6, its MW is: 19 kDa.

NON TER 5 5
SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flengsrud R., Skjeldal L.;
"Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum WS.";
Electrophoresis 19:802-806(1998).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Unknown protein CP 6 from 2D-page (Fragment).
Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDLINE=89008313; PubMed=3139658;
Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunny G.M., Suzuki A.;
"Structure of cCF10, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline resistance plasmid, pCF10.";
                                                                                                                                                                                                                                    27.3%; Score 9; DB 1; Length 5; 66.7%; Pred. No. 1.4e+05; tive 0; Mismatches 1; Indels
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MEDLINE=98291870; PubMed=9629918;
                                                                                                                                                                                                                                  Query Match 27.3;
Best Local Similarity 66.7;
Matches 2; Conservative
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UNO6_CLOPA
ID UNO6_CLOPA
AC P81351;
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CCF1_ENTFA
            STAGETTONES
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-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
-cyclohydrolase I. This inhibition is reversed by L-phenylalanine
(By similarity).
-!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.",
Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GERP MOUSE STANDARD; PRT; 7 AA.
P99025;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GCHFR OR GFRP.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UF01_MOUSE STANDARD; PRT; 5 AA.
P38639;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.;
                                                                                                                                                                                                                                               / Match 33.3%; Score 11; DB 1; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+05; Nes 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 30.3%; Score 10; DB 1; Length 7; Best Local Similarity 75.0%; Pred. No. 1.4e+05; Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 806 MW; 71B5B057273B4700 CRC64;
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SEQUENCE.
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Best Local S
Matches 2
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SEQUENCE

RESULT 4
UF01_MOUSE
ID _UF01_MC
AC P38639:
DT 01-OCT
DT 15-MAR
DE UNKNOW
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Gaps

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GenCore version 5/1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model 🗡

June 1, 2004, 10:41:50; Search time 7.66667 Seconds (without alignments) 47.542 Million cell updates/sec Run on:

US-09-712-819C-6 33 1 FTLKISR 7 Title: Perfect score: Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	72 litoria rub	3 litoria	'n	enm snm 6	1 clos	-41	01 alcaligenes	Δ1	10 zea mays (m	carc /		carcinu	6 carcinus ma	7 carcinus ma	~	œ	0	4 hirudo m	vibrio	_) herpes s	l achatir	^	_	5 anthopleura		7 anthopleura					_	~
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	ΩI	RE31	RE32_LITRU	GFRP_MOUSE	UF01_MOUSE	UNOG_CLOPA	CCF1_ENTFA	CHOX_ALCSP	CIA_ENTFA	UC24_MAIZE	AL14_CARMA	PSK_DAUCA	ALL2_CARMA	JARMA	CARMA		. ALL7_CYDPO P						ACHFU	FAR3_HIRME	FAR4_HIRME	FFKA_ANTEL	FLRF_HIRME	FLRN_ANTEL	FMRF_MACNI	FYRI_ANTEL	OCP1_OCTMI	ITRU	IO4_LITRU	ARTTR
	EQ (,						-			-	-	-	-	_	-	_	_	_	-	-	-	-			н	rd 	⊢ 1	Н			Н	H	Н
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dφ	Query Match		m	ö		7.		27.3	Ľ.	ζ.	4,	4.	4.	47	24.2	귝.	4,	24.2	4,		H	H 1	ω.	18.2	00	œ.	œ	œ	φ.	ω.	18.2	18.2	18.2	18.2
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/ Match 33.3%; Score 11; DB 1; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+05; Los 2; Conservative 0; Mismatches 0; Indels

Query Match

1 FT 2

ठ 윱 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
NCBI TaxID=104895;

RE32_LITRU
AC P82073;
DT 28-FEB-2003 (1)
DT 28-FEB-2003 (1)
DT 28-FEB-2003 (1)
DF Nubellidin 3...
OS Litoria rubel.
OC Pukaryota; Met
OC Amphibia; Batio
OC Pelodryadinae
OX NCBI_TaxID=10.
RN (1)
RP SEQUENCE.
RC TISSUE=Skin se

TISSUE=Skin secretion;

5 AA.

PRT;

STANDARD;

PAPP2 PARMA REII_LITRU SUGA_ACHDO TPIS_CANFA TOCOTA_MAIZE ACCOPTA_MATED CIP2_MYTED CIP2_	P81864 pardachirus P82070 litoria rub P82071 litoria rub P19991 acheta dome P54714 canis famil P80628 zea mays (m P25154 oryctolagus P13736 mytilus edu P82096 litoria rub P41966 moniezia ex		ata; Euteleostomi; dea; Hylidae;	I., Bowie J.H., Gao C., Australin red tree frog Le as a probe for the study activity nor antibiotic skin dorsal glands.
6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 6 18.2 7-2003 (Rel. 41, 7-2003 (Rel. 42, 11din 3.1. 1-2003 (Rel. 41, 7-2003 (Rel. 41, 7-2003 (Rel. 41, 7-2003 (Rel. 42, 11din 3.1. 1-2003 (Rel. 41, 7-2003 (Rel. 41, 7-2003 (Rel. 42, 11din 3.1. 1-2003 (Rel. 41, 7-2003 (Rel. 42, 11din 3.1. 1-2003 (Rel. 41, 7-2003 (Rel. 42, 1-2003 (Rel. 41,	ннанананан	e e t t	t tree frog). Ordata; Craniata; Vertebra Anura; Neobatrachia; Hyloio 	P.A., Waugh R.d. ides from the A m peptide profit amphibians."; 1996; Ir neuropeptide Secreted. Secreted. Secreted. Amidation. 71A9C9CB103000
RESULT 1 RESULT		LITRU STANDAR 2, B-2003 (Rel. 41, B-2003 (Rel. 41,	Rubellidin 3.1. Litoria rubella (Desert Eukaryota; Metazoa; Cho Amphibia; Batrachia; An Pelodryadinae; Litoria. NCBI_TaxID=104895; [1] SEQUENCE, AND MASS SPEC TISSUE=Skin secretion;	Steinborner S.T., Wabnitz Tyler M.J., Wallace J.C.; "The structure of new pept 'Litoria rubella'. The ski of evolutionary trends of Aust. J. Chem. 49:955-963' -!- FUNCTION: Shows neithe activity!- SUBCELLULAR LOCATION: -!- TISSUE SPECIFICITY: EX!- TISSUE SPECIFICITY: EX!- MASS SPECTROMETRY: MW- Amphibian defense peptide; MOD RES SEQUENCE 5 AA; 656 MW;

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T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0577; PT0574
R;Feeney, A.J.
J; Exeney, A.J.
J; Exeney, A.J.
J; Exeney, A.J.
J; Exeney, A.J.
J; Exeney: Muctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Reference number: PT0509
A;Reference number: PT0509
A;Reference number: PT0574
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
A;Residues: 1-5 <FE2>
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Teceptor beta chain V-D-J region (141-1CF) - mouse (fragment); Species: Mus musculus (house mouse); Species: Mus musculus (house mouse); Date: 17-Jul-1992 #text_change 30-May-1997; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997; Peeney, A.J.

Exp. Med. 174, 115-124, 1991

Exp. Med. 174, 115-124, 1991

Fritle: Junctional sequences of fetal T cell receptor beta chains have few N regions. Reference number: PT0509; MUID:91277601; PMID:1711558
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A;Molecule type: mRNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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Search completed: June 1, 2004, 11:19:23 Job time: 11.6667 secs ô

Gaps

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phosphoprotein, bone - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C;Accession: S11127; S11128
R;Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. J. 268, 585-591, 1990
A;Title: Post-translational processing of chicken bone phosphoproteins. Identificational procession: S11127; MUID:90303246; PMID:2363696
A;Accession: S11127
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <MIXI>
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0525
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regic A;Reference number: PT0509; MUID:91277601; PMID:1711558
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                                 A;Accession: A44955
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <PAQ>
C;Keywords: FMN; luminescence; monooxygenase; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 5;
               A; Reference number: A44955; MUID:90175700; PMID:2626493
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1,
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Pred. No. 2.8e+05;
2; Mismatches 0
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A;Molecule type: mRNA
A;Residues: 1-5 <FBE>
A;Experimental source: adult thymus, strain BALB/C
C;Keywords: T-cell receptor
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Best Local Similarity 33.3
Matches 1, Conservative
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A;Molecule type: protein
A;Residues: 'X',2-5 <MIK2>
C;Keywords: phosphoprotein
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3 VSK 5
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PT0577
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                                                                                                                                                                                                                                                                                                                                                                                glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A60521.
A; Molecule type: protein
A; Residues: 1-5 < BON>
C; Superfamily: glucan phosphorylase
C; Superfamily: glucan phosphorylase
C; Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F; 3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    figure protein flik - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq A;Reference number: A42364; MUID:91258342; PMID:1646201
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VOG>A;Cross-references: GB:M62408
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C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 26-May-2000
C;Accession: A44955
R;Paquatte, O.; Tu, S.C.
R;Paquatte, O.; Tu, S.C.
Photochem. Photobiol. 50, 817-825, 1989
A;Title: Chemical modification and characterization of the alpha cysteine 106 at the Vib
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                                                                                                                                             0; Indels
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2x86PT3; 8 month seedlings
                                                                                   Score 9; DB 2; Length 4;
Pred. No. 2.8e+05;
2; Mismatches 0; Indel
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                                                                                th 27.3%;
Similarity 33.3%;
1; Conservative 2
                                                                       Ouery Match
Best Local Similarity
Matches 1; Conserv
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Cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion Lampetra fluviatilis (river lamprey)
C; Species: mitochondrion Lampetra fluviatilis (river lamprey)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: T13892
R; Delarbre, C:; Barriel, V:; Tillier, S:; Janvier, P:; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A; Title: The main features of the craniate mitochondrial DNA between the ND1 and the A; Reference number: Z17775; MUID: 97398704; PMID: 9254918
A; Reference number: Z17775; MUID: 97398704; PMID: 9254918
A; Reference sin preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-3 < DEL>A; Cross-references: EMBL: Y09528; NID: 92340016; PIDN: CAA70721.1; PID: 94379123
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cispecies: Clostridium thermocellum (fragment)
Cispecies: Clostridium thermocellum
Cispecies: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Aug-1996
Ciscossion: 140804
Rimishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 1991
A;Title: Transcription of clostridium thermoncellum endoglucanase genes celf and cisperence number: 140804; MUID:91100322; PMID:1987137
A;Reference number: 140804
A;Reference number: 140804
A;Residues: 1-4 <RES>
A;Residues: 1-4 <RES>
A;Cross-references: GB:M64363; NID:g144771
C;Genetics:
A;Genetics:
A;Genetics:
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C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and
A;Accession: T46627
A;Accession: T46627
A;Molecule type: mRNA
A;Residues: 1-4 <CHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Genome: mitochondrion
A,Note: COI
C,Keywords: mitochondrion; oxidoreductase
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T14910
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14910
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14910
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5 < KIR>
A;Residues: 1-5 < KIR>
A;Experimental source: ssp. Hamburger Schnitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Procedure Transcript of the parachain V-D-J region (111-1G) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0644
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0644
A; Reference number: PT0644
A; Accession: PT0644
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-5 < FEE>
A; Experimental source: newborn thymus, strain BALB/C
C; Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: O3-Feb-1994 #sequence_revision O3-Feb-1994 #text_change 23-Mar-1995
C;Accession: PS0254
R;Tsugita, A.
submitted to JIPID, April 1993
A;Reference number: PS0206
A;Accession: PS0254
A;Molecule type: protein
A;Residues: 1-7 <TSU;
A;Experimental source: leaf, chloroplast, strain Nihonbare
A;Note: molecular weight 18K, pI 4.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 36.4%; Score 12; DB 2; Length 5; Local Similarity 66.7%; Pred. No. 2.8e+05; nes 2; Conservative 1; Mismatches 0; Indels
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GenCore version 5/1/6.
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 1, 2004, 10:56:46; Search time 11.6667 Seconds (without alignments) 57.715 Million cell updates/sec Run on:

US-09-712-819C-6 33 1 FTLKISR 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

457 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribosomal protein	ര	hypothetical prote	T-cell receptor be	18K protein 5507 -		endoglucanase F -	hypothetical prote	glycogen phosphory	flagellar protein	alkanal monooxygen	phosphoprotein, bo	T-cell receptor be	T-cell receptor be	T-cell receptor be	T-cell receptor be	surface protein te	N-formyl oligopept	28K ubiquítin-immu	Y protein - human	alpha-1,4-glucan-p	MHC H2-L antigen -	T-cell receptor be	T-cell receptor be		peptidyl-dipeptida	choline oxidase (E	phosphotransferase	pilE protein - Esc
SUMMARIES	ΙD	819630	A28709	T14910	PT0644	PS0254	T13892	I40804	T46627	A60521	E42364	A44955	811127	PT0525	PT0577	PT0565	PT0700	S69237	A60986	A43766	137263	B26206	I65546	PT0518	PT0662	I49424	JN0859	A15398	B39127	S25266
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	Score	15		12			σ	ወ	ወ	σv	თ	თ	ω	σ	σ	σ	Q	თ	on	σ n	o,	ወ	σv	ወ	ጣ	σ	6	σ	σ	σı
	Result No.	н	7	m	4	ស	v	7	ω	o,	10	11	12	13	14	15	16	17	18	ტ -	50	21	22	23	24	25	56	27	28	0 0

phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C;Species: Bacillus cereus
C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C;Accession: A28709
R;Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evic

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Query Match 39.4%; Score 13; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels

3 LKI 5 LKI 3

ð P. RESULT

A,Reference number: A28709; MUID:88241058; PMID:3132206 A;Accession: A28709 A;Status: preliminary A;Molecule type: protein A;Residues: 1-7 <OLS>

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Search completed: June 1, 2004, 11:20:18 Job time: 14.6667 secs
                       1 TDF 3
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APPLICANT: Bearry S. Cooperman, Harvey Rubin,
APPLICANT: Bearry S. Cooperman, Harvey Rubin,
APPLICANT: Derone Salem, and Alison L. Fisher
TITLE OF INVENTION: "Pleamodium falciparum Ribonu-
TITLE OF INVENTION: Thereof"

TITLE OF INVENTION: Thereof"

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: The University of Pennsylvania
STREET: 3700 Market Street
CITY: Philadelphia
COUNTRY: U.S.A.
ADDRESSEE: IBM PS/S.
CONTYIR: BADBALE FORM:
MEDIUM TIPE: Diskette, 3.50 inch, 720 Kb
COMPUTER IBM PS/S.
COMPUTER IBM PS/S.
COMPUTER IDM PS/S.
COMPUTER IDM PS/S.
COMPUTER IDM PS/S.
ATTORNEY/ABATION DATA:
PTILING DATE: 10/14/93
ATTORNEY/ABATION WORDER: 3957-10
TELECOMMUNICATION WORDER: 3957-10
TELECOMMUNICAT
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Sequence 31, Application US/08136743B
Patent No. 5459063
GENERAL INFORMATION:
FILING DATE: 10/14/93
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 3957-
TELECOMMUNICATION INFORMATION:
TELECHONE: (215) 568-8383
TELEX: NO. 54590636
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 3; Conservative
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; TOPOLOGY: linear
US-08-136-743B-31
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APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Barry S. Cooperman, Harvey Rubin,
TITLE OF INVENTION: "Pleancdium falciparum Ribonu-
TITLE OF INVENTION: Theoride Reductase, DNA Sequences Therefor and Peptide in
NUMBER OF SEQUENCES: 67
CONRESPONDENCE ADDRESS;
ADDRESSEE THE University of Pennsylvania
STREET: Suite Pennsylvania
COUNTRY: U.S.A.
STREET: Suite Pennsylvania
COUNTRY: U.S.A.
STREET: Diskette, 3.50 inch, 720 Kb
COMPUTER: READABLE PORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: BEADABLE PORM:
MEDIUM TYPE: US/08/136,743B
FILING DATE: 10/14/93
CLASSIFICATION: 435
ATTORNENT APPLICATION DATA:
APPLICATION NUMBER: 3957-10
FILING DATE: 10/14/93
CLASSIFICATION: NUMBER: 3957-10
TELESCOMMUNCATION INFORMATION:
NAME: NORACY NUMBER: 3957-10
TELESTRAICATION NUMBER: 3957-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 30, Application US/08136743B
; Patent No. 5459063
; GENERAL INFORMATION:
    APPLICANT: Barry S. Cooperman, Harvey Rubin,
    APPLICANT: Barry S. Cooperman, Harvey Rubin,
    APPLICANT: Barry S. Cooperman, Harvey Rubin,
    TITLE OF INVENTION: "Pleamodium falciparum Ribonu-
    TITLE OF INVENTION: "Pleamodium falciparum Ribonu-
    TITLE OF INVENTION: "Pleamodium falciparum Ribonu-
    TITLE OF INVENTION: "Phereof"
    TITLE OF INVENTION: Thereof"
    TITLE OF INVENTION: Thereof,
    TITLE OF INVENTION: THE TABLE FORM:
    TITLE OF INVENTION: THE TABLE FORM:
    MEDIUM TYPE: THE PASSABLE FORM:
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 3; Conservative
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US-08-136-743B-30
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                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
FRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1133
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 271
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h Similarity 100.0%; Pred. No. 3e+05; 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09233857;
Patent No. 6495353;
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
APPLICANT: Planagan, Peter
TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
FILE REFERENCE: 239/251
CURRENT FILING DATE: 1999-01-20;
EARLIER APPLICATION NUMBER: US/09/233,857
CURRENT FILING DATE: 1999-01-20;
EARLIER FILING DATE: 1998-01-21;
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-271
                                                                                                                                                                                      Sequence 271, Application US/09428082B Patent No. 6660843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 29, Application US/08136743B Patent No. 5459063 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserva
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CRGANISM: HUMAN
US-09-233-857-7
                                                                                                                                                           US-09-428-082B-271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-136-743B-29
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US-09-233-857-7
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Gaps

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Schlokat, Uwe
Schlokat, Uwe
Dorner, Friedrich
Fisch, Andreas
Eibl, Johann
TITLE OF INVENTION: Factor X Analogues With
a Modified Protease Cleavage Site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.6%; Score 17; DB 4; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/367,791A
FILING DATE: 12-No. 6573071-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,471
REFERENCE/DOCKET NUMBER: 20695D-000700US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                         Score 17; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 335/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00045
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                           Query Match 48.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 3e4 Matches 3; Conservative 0; Mismatches
                             STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-09-367-777-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-367-791A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Himmelspach, Michele
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76, Application US/09367791A
Patent No. 6573071
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 76: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
LOCATION: 1..5
OTHER INFORMATION: /note= "Amino acid sequence
OTHER INFORMATION: encoded by nucleotides 1-15 of SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.6%; Score 17; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATION
SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRING DATE: 10-NO. 6562598-1999
CLASSIFICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
COMPATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000900US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlokat, Uwe
TITLE OF INVENTION: Factor X Deletion Mutants
and Analogues Thereof
REFERENCE/DOCKET NUMBER: 001560-215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESUL: >
US-09-367-777-132

Sequence 132, Application US/09367777

Patent No. 6562598

GENERAL INFORMATION:

APPLICANT: Himmelspach, Michael

Himmelspach, Michael

Ealkner, Falko-Guenter

Bibl, Johann

Dorner, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 145
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APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: TANIGUCHI, Nacyuki
APPLICANT: NISHIKAWA, Aksushi
APPLICANT: YAMAGUCHI, No. 5707846cmi
APPLICANT: YAMAGUCHI, No. 5707846cmi
APPLICANT: YAMAGUCHI, No. 5707846cmi
TITLE OF INVENTION: NOVEL N-ACETYLGLUCOSAMINYL TRANSFERASE
TITLE OF INVENTION: GENE CODING THEREFOR AND PROCESS FOR PRODUCTION THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDERS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STATE: Virginia
COUNTRY: United States
ZIF: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIF: 22313-1404
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/405,230
FILING DATE: L6-MAR-1995
FILING DATE: 23-AUG-1993
APPLICATION NUMBER: US 4-245950
FILING DATE: 23-AUG-1992
FILING DATE: 24-AUG-1992
                                                                                                                                                                                                                                             Patent No. 6420120.

GENERAL INFORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
TITLE OF INVENTION: USe 0.32751-036
CURRENT APPLICATION NUMBER: US/09/155,613A
CURRENT APPLICATION NUMBER: PCT/FR98/00184
PRIOR FILING DATE: 1998-01-30
PRIOR FILING DATE: 1997-01-30
PRIOR PRIOR FILING DATE: 1997-01-30
PRIOR FILING DATE: 1997-01-30
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                                                                                                                                              RESULT 6
US-09-155-613A-59
; Sequence 59, Application US/09155613A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-405-230-10
; Sequence 10, Application US/08405230
; Patent No. 5707846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Phagotope US-09-155-613A-59
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1 FTLSV 5
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2 NYTLT 6
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JEAURING DATE: US/08910900

JEAURING OND STATES

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-237118
PILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 001560-215
TELECHONE: (703) 836-6620
TELEPHONE: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TOF 3
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US-08-910-990-10
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lo, Reggie Y.C.
APPLICANT: Schryvers, Anthony B.
APPLICANT: Schryvers, Andrew A.
TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
TITLE OF INVENT PILLING DATE: 1996-11-29
CURRENT FILLING DATE: 1996-11-29
PRIOR APPLICATION NUMBER: CA 2,164,274
PRIOR FILLING DATE: 1995-12-01
PRIOR FILLING DATE: 1995-12-01
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 7
                       APPLICANT: HELLYER, Susan A.
APPLICANT: DE SILVA, Jacqueline
APPLICANT: WHITEMAN, Sally A.
TITLE OF INVENTION: Tomato Xyloglucan Endo-Transglycosylase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                    NUMBER OF SEQUENCES: "."

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,737
FILING DATE: 10-MOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9323225.4
FILING DATE: 10-NOV-1993
INPORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 3;
Pred. No. 3e+05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 19; DB 4;
Pred. No. 3e+05;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08753750B Patent No. 6610506
   ARROWSMITH, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.3%;
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Best Local Similarity 80.00
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, ORGANISM: Escherichia coli
US-08-753-750B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                            Patent No. 6001986
GENERAL INFORMATION:
APPLICANT: Yong Sig KIM
APPLICANT: Sun Chung PARK
APPLICANT: Soo Kyung OH
APPLICANT: Hosull LEE
APPLICANT: Jeong Woo CHO
APPLICANT: Chang H. CHUNG
TITLE OF INVENTION: Antiviral Proteins, Amarandin 1 and 2, from
TITLE OF INVENTION: Amaranthus Viridis, DNAs Encoding Therefrom
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                 ;
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                                                                                      Score 19; DB 4; Length 6;
Pred. No. 3e+05;
0; Mismatches 1; Indels
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Pred. No. 3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W., Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: 3+ Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: WordPerfect 6.1 Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,443A
FILING DATE: 22 AUG 1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                            8, Application US/08916443A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 38, Application US/08640737; Patent No. 6215044; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Toffenetti, Judith L.
REGISTRATION NUMBER: 39,048
REFERENCE/DOCKET NUMBER: 1942
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-429-1776
; LOCATION: ()...(); CTHER INFORMATION: Epitope tag US-09-724-297-4
                                                                                  Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 8:
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Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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US-08-640-737-38
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0; Indels Length 7;

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Sequence 4, Appli
Sequence 8, Appli
Sequence 20, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 23, Appli
Sequence 14, Appl
Sequence 23, Appli
Sequence 14, Appl
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appl
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 26, Appli
                                                                                                                          June 1, 2004, 11:13:51; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-724-297-4
US-08-916-443A-8
US-08-640-737-38
US-08-640-737-38
US-08-753-750B-20
US-09-155-613A-59
US-08-915-613A-59
US-08-910-990-10
US-09-367-770-132
US-09-367-771-32
US-09-367-771-32
US-09-367-771-32
US-09-367-771-32
US-08-136-743B-29
US-08-136-743B-31
US-08-136-743B-31
US-08-136-743B-32
US-08-136-743B-32
US-08-136-743B-32
US-08-136-743B-32
US-08-136-743B-32
US-08-136-743B-32
US-08-136-743B-32
US-08-136-739-401A-6
PCT-US93-11703-72
US-08-136-739-401A-6
PCT-US93-11703-72
US-08-591-632-23
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US-08-591-632-23
US-08-591-632-23
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                                                                                                                                                                                                                                                                                                                                                                             389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score: 3
Sequence: 1
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No.
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Sequence 14, Appl Sequence 23, Appl Sequence 23, Appl Sequence 14, Appl Sequence 17, Appli Sequence 17, Appli Sequence 1745, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22, Appli Sequence 52, Appli Sequence 1746, Appli	Proteins and Uses Thereof	ength 6; Indels 0; Gaps 0;	y of Illinois Froteins and Uses Thereof
5 4 US-09-166-205B-14 5 4 US-09-611-451-17 5 4 US-09-611-451-23 5 4 US-09-611-451-26 5 5 PCT-US94-02629-14 6 1 US-08-252-95D-7 6 2 US-08-834-108-7 6 2 US-08-834-108-7 6 3 US-08-834-108-7 7 1 US-08-136-946-5 7 2 US-08-177-109A-7 7 2 US-08-177-109A-7 7 3 US-09-040-216-28 7 4 US-09-535-852-1746	ALIGNMENTS 140084A 11 Surface Display of US/09/140,084A -26 ion of Unknown Organi	54.3%; Score 19; DB 4; L 80.0%; Pred. No. 3e+05; ive 0; Mismatches 1;	on US/09724297 d of Trustees of the University et al. Yeast Cell Surface Display of -99C NUMBER: US/09/724,297 2000-11-28 MBER: US 09/009,388 1998-01-20 : 26 version 3.0
28 30 31 32 33 34 33 34 35 36 37 36 46 47 47 47 47 47 47 47 47 47 47	RESULT 1 US-09-140-084-4 ; Sequence 4, Application US/09: ; Patent No. 6300065 ; GENERAL INFORMATION: ; APPLICANT: Kieke, et al.; ; TITLE OF INVENTION: Yeast Ce.; ; FILE REFERENCE: D6061CIP2; ; CURRENT APPLICATION NUMBER: UCRRENT FILING DATE: 1998-08; ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 4 ; LENGTH: 6 ; CORGANISM: Unknown ; FEATURE: ; OTHER INFORMATION: Descript: US-09-140-084-4	Query Match Best Local Similarity Matches 4; Conservat Qy TDFTL 5	RESULT 2 US-09-724-297-4 US-09-724-297-4 Sequence 4, Application US/097 Batent No. 642338 GENERAL INFORMATION: APPLICANT: The Board of Trus APPLICANT: Witrup, et al. TITLE OF INVENTION: Yeast C FILE REFERENCE: 97-99C CURRENT APPLICATION NUMBER: U PRIOR APPLICATION NUMBER: U PRIOR APPLICATION NUMBER: U PRIOR APPLICATION NUMBER: U BRIOR PILING DATE: 1998-01-01 NUMBER OF SEQ ID NOS: 26 SOFTWARE: PATENTI NOS: 26 TYPE: PRT CORGANISM: unknown FEATURE: NAME/KEY: misc_feature

us-09-712-819c-5.closed.rapb

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APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: DU-0007
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT APPLICATION DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REPERENCE: PU-0007
CURRENT APPLICATION NUMBER: US/09/788,006
CURRENT APPLICATION DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 5
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Query Match 51.4%; Score 18; DB 14; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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Pred. No. 1e+06;
1; Mismatches 0; Indels
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Pred. No. 1e+06;
1; Mismatches 0; Indels
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Job time : 35.6667 secs
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Publication No. US20030036093A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Streptomyces griseus
US-09-788-006-108
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0%;
Matches 3; Conservative
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US-09-788-006-107
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US-09-788-006-108
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SEQ ID NO 11
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Publication No. US20020150558A1

GENERAL INFORMATION:

APPLICANT: Boulanger, Pierre

APPLICANT: Hong, Saw See

APPLICANT: Asaryan, Lucie

TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses

FILE REFERENCE: 032751-036

CURRENT FILING DATE: 2002-06-30

PRIOR FILING DATE: 1998-01-30

PRIOR FILING DATE: 1997-01-30

PRIOR FILING DATE: 1997-01-30

PRIOR FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 98

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO S9
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APPLICANT: Mazur, Wieslaw A

TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M

CURRENT APPLICATION NUMBER: US/10/317,252A

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: US 60/349,117

PRIOR PILING DATE: 2002-01-16

PRIOR PELING DATE: 2002-04-29

PRIOR FILING DATE: 2002-04-29

PRIOR FILING DATE: 2002-04-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 530

SOFTWARE: Patentin version 3.2

SEQ ID NO 402

LENGTH: 6

PLENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 14; Length 6; Pred. No. 1e+06; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 51.4%; Score 18; DB 13; Length 6; Best Local Similarity 60.0%; Pred. No. 1e+06; Matches 3; Conservative 2; Mismatches 0; Indels
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US-10-267-565-11
; Sequence 11, Application US/10267565
; Publication No. US20030204059A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%;
80.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Phagotope
US-10-156-820-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: artificial FEATURE:
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US-10-156-820-59
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Sequence 11, Application US/10349507

| Sequence 11, Application US/2030199002A1
| Publication No. US20030199002A1
| GENERAL INFORMATION:
| APPLICANT: Hekimi , Siegfried
| APPLICANT: Hekimi , Siegfried
| APPLICANT: Brand, Hania |
| APPLICANT: Brand, Hania |
| APPLICANT: McCright, Brenton |
| APPLICANT: Lakowski , Bernard |
| APPLICANT: Lakowski , Bernard |
| TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF |
| TITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF |
| TITLE OF INVENTION NUMBER: US/10/349,507 |
| CURRENT FILING DATE: 2003-01-22 |
| PRIOR PILING DATE: 2001-06-20 |
| PRIOR PLIING DATE: 2000-06-22 |
| PRIOR PILING DATE: 2000-06-22 |
| PRIOR PILING DATE: 2000-12-13 |
| PRIOR APPLICATION NUMBER: 60/213,174 |
| PRIOR APPLICATION NUMBER: 60/254,932 |
| PRIOR PILING DATE: 2000-12-13 |
| NUMBER: COND-12-13 |
| NUMB
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APPLICANT: Gubler, Untrich
APPLICANT: Gubler, Untrich
APPLICANT: Hulmes, Jeffery
APPLICANT: Hulmes, Jeffery
APPLICANT: Hulmes, Jeffery
APPLICANT: Stern, Alvin
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
FILE REPERENCE: 11126-05
CURRENT FILING DATE: 1990-09-22
PRIOR FILING DATE: 1990-09-22
PRIOR FILING DATE: 1990-08-27
PRIOR FILING DATE: 1990-08-27
PRIOR FILING DATE: 1990-08-27
PRIOR FILING DATE: 1990-05-09
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SOFTWARE: Patentin version 3.2
SEQ ID NO 11
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US-10-267-565-11
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; ORGANISM: Homo sapiens
US-10-349-507-11
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Gaps

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Sequence 402, Application US/10317251A;
Sequence 402, Application US/10317251A;
Publication No. US20030148957A1;
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company;
APPLICANT: Talsfort, Wieslaw A;
ITILE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists;
ILIE REFERENCE: 8847M2
CURRENT APPLICATION NUMBER: US/10/317,251A;
CURRENT FILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-315-964A-402
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; OTHER INFORMATION: Chemically synthesized artificial peptide
US-10-317-251A-402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.3%; Score 19; DB 14; Length 6; Best Local Similarity 80.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 1; Indels
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  PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/376,337
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-04-29
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-19
PRIOR PILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 402
LENGTH: 6
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APPLICANT: The Procter & Gamble Company APPLICANT: Isfort, Robert J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: artificial
FEATURE:
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TKFTL 6
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US-10-317-252A-402
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Sequence 4, Application US/10083815

Publication No. US20030026781A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Clevenger, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING

TITLE OF INVENTION: ENDOGENOUS INHIBITOR OF ATP SYNTHASE, INCLUDING

TITLE OF INVENTION: TREATMENT FOR DIABETES

FILE REFERENCE: 660088.435C2

CURRENT APPLICATION NUMBER: US/10/083,815

CURRENT FILING DATE: 2002-02-27

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                       APPLICANT: Clevenger, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATING
TITLE OF INVENTION: TREATMENT FOR DIABETES
TITLE OF INVENTION: TREATMENT FOR DIABETES
FILE REFERENCE: 660088.435C1
CURRENT APPLICATION NUMBER: US/09/796,076
CURRENT FILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6
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Sequence 402, Application US/10315964A
Publication No. US20030148956A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M3
CURRENT APPLICATION NUMBER: US/10/315,964A
CURRENT FILING DATE: 2003-04-01
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Best Local Similarity 80.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels
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Publication No. US20040072739A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: Epitope tag
US-09-796-076-4
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US-10-083-815-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
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APPLICANT: Isfort, Robert J
APPLICANT: Isfort, Robert J
APPLICANT: Isfort, Robert J
APPLICANT: Mazur, Wieslaw A
TITLE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M2
CURRENT APPLICATION NUMBER: US/10/317,251A
CURRENT FILING DATE: 2002-12-11
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-04-29
PRIOR FILING DATE: 2002-09-19
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: Patentin version 3.2
SEQ ID NO 394
LENGTH: 5
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Mazur, Wieslaw A
VENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Chemically synthesized artificial peptide US-10-315-964A-394
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    APPLICANT: Mazur, missing.

TITLE OF INVENTION: Cortcotropin Releasing Fac
FILE REFERENCE: 8847M3

CURRENT APPLICATION NUMBER: US/10/315,964A

CURRENT FILING DATE: 2003-04-01

FRIOR APPLICATION NUMBER: US 60/349,117

PRIOR FILING DATE: 2002-01-16

PRIOR FILING DATE: 2002-04-29

PRIOR FILING DATE: 2002-04-29

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-06-14

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 530

SOFTWARE: Patentin Version 3.2

LENGTH: 5

LENGTH: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: artificial
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RESULT 4 US-10-317-252A-394

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Sequence 122, Application US/10351891
; Sequence 122, Application US/20040048311A1
; Publication No. US20040048311A1
; GENERAL INFORMATION:
; APPLICANT: DANA AULT-RICHE
; APPLICANT: PAUL D. KASSNER
; TITLE OF INVENTION: USE OF COLLECTIONS OF BINDING SITES FOR SAMPLE PROFILING AN
; FILE REFERENCE: 25885-1753
; CURRENT APPLICATION NUMBER: US/10/351,891
; CURRENT APPLICATION NUMBER: US 60/352,011
; PRIOR APPLICATION NUMBER: US 60/352,011
; PRIOR FILING DATE: 2002-01-24
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 6
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Sequence 394, Application US/10317252A

Publication No. US20030148958A1

GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: The Procter US
APPLICANT: Macur, Wieslaw A

ITILE OF INVENTION: Cortcotropin Releasing Factor 2 Receptor Agonists
FILE REFERENCE: 8847M
CURRENT APPLICATION NUMBER: US/10/317,252A

CURRENT APPLICATION NUMBER: US 60/349,117
PRIOR APPLICATION NUMBER: US 60/349,117
PRIOR FILING DATE: 2002-01-16
PRIOR FILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-06-14
PRIOR PILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 530
SOFTWARE: PatentIn version 3.2
SEQ ID NO 394
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US-10-317-252A-394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 19; DB 14; Length 5; 80.0%; Pred. No. 1e+06; 1; Indels iive 0; Mismatches 1; Indels
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Pred. No. 1e+06;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: AUS Peptide US-10-351-891-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: artificial
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US-09-796-076-4
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Sequence 126, App
Sequence 394, App
Sequence 394, App
Sequence 394, App
Sequence 122, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 402, App
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Sequence 402, App
Sequence 59, Appl
Sequence 11, Appl
Sequence 11, Appl
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Sequence
Sequence
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-315-964A-394
US-10-317-251A-394
US-10-317-252A-394
US-10-351-891-122
US-09-76-4
US-10-083-815-4
US-10-315-964A-402
US-10-317-251A-402
US-10-317-257-11
                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                          1151071 segs, 279249464 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                        US-09-712-819C-5
35
1 TDFTLTI 7
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 7
                                                                                                                                                                                                                          Title:
Perfect score:
Sequence:
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Maximum DB seq
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                                                                                                                                     Run on:
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No.
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Sequence 151, App	7	Ŋ	e 2	271,	equence 271,	132	76, 4	equence 271	27	Ñ	-	Sequence 25, Appl	S	28	12	equence 5,	O	Sequence 93, Appl	Ψ	equence 2	equence 3	(.4	equence 3	4	æ	equence 8	equence 7	m	equence
6-549-1	-549-2	US-10-609-217-271	2-388-2	1-7	-10-645-761-2	0-348-504-1	-10-407-123-	-10-666-696-2	10-653-048-2	-102A	S-10-284-130-	72-9	-09-954-38	-10 - 264 - 30	-10 - 380 - 53	0-286-993-	-832-723-	0-080-0	0-303-331-	9-788-006	8-006-	0-214-796-	0-286-18	0-286-18	US-09-293-854-8	S-09-990-586-	US-10-400-991-75	S-10-105-930-	-869-6
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17			17		17	11		17		17		17	17	17	16	16	16	16	16	15	15	15	15	15	15	15	15	15	15
16	17	18	61	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Ptashne, et al.,
TITLE OF INVENTION: Transcriptional Activation System, Activators, and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: 0342941-0065
CURRENT APPLICATION NUMBER: US/09/943,944E
CURRENT FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 126
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence:Random peptide; OTHER INFORMATION: sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 20; DB 11; Length 6; 80.0%; Pred. No. 1e+06; rative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-315-964A-394
; Sequence 394, Application US/10315964A
; Publication No. US20030148956A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Isfort, Robert J
US-09-943-944E-126; Sequence 126, Application US/09943944E; Publication No. US20040014036A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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XX SQ Sequence 6 AA;

Query Match 54.3%; Score 19; DB 3; Length 6; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 1; Indels

Search completed: June 1, 2004, 11:16:16 Job time: 47.6667 secs

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                                                                                                                                                                                                             This peptide comprises an epitope tag that can be used in methods of the invention. The invention discloses a powerful new system for engineering antibody affinity and specificity, by constructing a microbial analogue of the mammalian system's B cell repertoire. Antibodies are displayed on the surface of yeast cells by genetic fusion with yeast cell wall proteins, especially agglutinin proteins. After mutation, variants are selected on the basis of improved binding characteristics with fluorescently labeled targets. The selection method also identifies proteins with enhanced phenotypic characteristics, proteins that are displayed at higher levels, proteins that are secreted at higher efficiency and proteins of improved stability
                                                                                                                                          Selecting proteins with enhanced phenotypic properties than wild-type proteins, is useful for highly specific cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Selecting proteins with enhanced phenotypic properties than wild-type proteins, is useful for highly specific cancer diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast cell wall protein; AGA2; T cell receptor; multiple sclerosis; cancer; sepsis; autoimmune disease; arthritis; diabetes.
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Pred. No. 1.4e+06;
0; Mismatches 1; Indels
                                                                                       Boder ET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epitope tag #2 fused to yeast cell wall protein AGA2.
                                                                                     Shusta E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boder
                                                                                                                                                                                      Disclosure, Page 7; 116pp, English.
                                                                                       Kranz DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE16558 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 40; Col 60; 59pp; English.
              98US-00009388.
98US-00140084.
                                                                                                                                                                                                                                                                                                                                                                                                                      54.3%;
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97US-00866398.
                                                      (UNII ) UNIV ILLINOIS FOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                    Wittrup KD, Kieke MC,
                                                                                                                WPI; 1999-430619/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-430619/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TOFTL 5
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6 AA;
             20-JAN-1998;
26-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1996;
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The present invention relates to a method for selecting proteins for displayability on a yeast cell surface. The method comprises transforming yeast cells with a vector that expresses a test protein fused to a yeast cell wall protein (AGA2), contacting the cells with a label that binds to proteins displayed on the cell wall, and isolating label-bound cells, where the test protein is from a variegated population generated by mutagenesis. The invention is also directed to new processes for engineering T cell receptor for improved binding properties. Improved T cell receptor molecules are useful in therapies for cancer, sepsis, autoimmune diseases such as arthritis, diabetes or multiple sclerosis. The methods are useful to select proteins with altered affinity, altered specificity or conditional binding. The present sequence is an epitope tag fused between protein of interest and yeast cell wall protein AGA2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a method for identifying compounds which inhibit internalization of cell surface receptors. Provided are an array of locations, each containing cells with a cell surface receptor protein, that are treated with a test compound. The protein is luminescently labeled or contacted with a luminescently labeled cell before or after test compound treatment. Any luminescence produced is converted into digital data and automatically analysed to determine if the test compound induced the protein internalization. The novel method is used to screen for compounds which modulate cell surface receptor protein internalization, this can be used in drug discovery, to test compound efficacy in living biological systems. The assay method is automated and compact. It has high throughput and uses smaller volumes of reagents and test compounds. Sequences AAY77704-718 represent examples of peptide epitope tags used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Automated screening method for identifying compounds which induce cell surface receptor internalization, useful for drug discovery.
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                              Length 6;
                                                                                                                                                                                                                                                                                                                         54.3%; Score 19; DB 2; I
80.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gough A, Dunlay T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 67; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY77708 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rubin RA, Giuliano KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELLOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-171170/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUS peptide epitope
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                                                                                                                                                                                                                                                                                     Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY77708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (GRF2). The CRF2 peptides have the following activities: myopathic, osteopathic, hypotenaive, cardiant, vasotropic, antidiabetic, analgesic, antiallergic, tranquilizer, anxidiabetic, analgesic, antiallergic, tranquilizer, anxidytic, antidepressant, and antiarthritic. The CRF2 peptides, and crelated compounds derived from other proteins, are used to prevent or treat disorders modulated by the CRF2 receptor, e.g. skeletal muscle atrophy or wasting, and bone disorders, however caused, heart/circulatory diseases (e.g. hypertension, congestive heart failure, heart attack, reperfusion injury, migraine, stroke, memory loss, Alzheimer's disease, dementia); joint disorders (osteoarthritis or rheumatoid arthritis); ont disorders (osteoarthritis or rheumatoid arthritis); ont disorders (osteoarthritis or rheumatoid arthritis); low levels of adrenocorticotrophic hormone; anorexia nervosa; depression; also to reduce body temperature and to control appetite or cognitive function. Nucleic acids, optionally labelled, that encode the CRF2 peptides are used to synthesis and for recombinant production of CRF2 peptides are used to evaluate expression of the CRF2 peptides after gene therapy. This sequence represents a novel native CRF polypeptide of the invention.
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                                                                                                                                                                                                                                            New non-native peptide derived from corticotropin-releasing factor-2, useful for treatment and prevention of e.g. muscular atrophy, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRF2 non-native polypeptide, SEQ ID No 394.
                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 394; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE51377 standard; peptide; 5 AA.
                16-JAN-2002; 2002US-0349117P.
29-APR-2002; 2002US-0376337P.
14-JUN-2002; 2002US-0388895P.
19-SEP-2002; 2002US-0411988P.
                                                                                                                     (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2004 (first entry)
                                                                                                                                                             Isfort RJ, Mazur WA;
                                                                                                                                                                                                      VPI; 2003-787975/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
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The invention relates to a novel non-native peptide derived from corticotropin-releasing factor-2 (CRF2). The non-native CRF2 peptides have the following activities: myopathic, osteopathic, hypotensive, cardiant, vasotropic, antidipateic, carebroprotective, noctropic, cardiant, vasotropic, antidipateic, and antidipateic, and and bone disorders, however.

Caused, heart/circulatory diseases (e.g. hypertension, congestive heart attack, reperfusion injury, migraine, stroke, memory loss, fallure, heart attack, reperfusion injury, migraine, stroke, memory loss, allery, stress; anxiety, low levels of acrencontricotrophic hormone; anorexia nervosa; depression; also to reduce body temperature and to control appetite or cognitive function. Nucleic acids, optionally and probes for amplification, also for gene synthesis and for recombinant control of the non-native CRF2 peptides are used as primers and probes for amplification, also for gene synthesis and for recombinant therapy. Antibodies specific for the non-native CRF2 peptides after gene therapy.

This sequence represents a CRF2 non-native polypeptide of the invention.
                                                                                                                                                                                                                                                          New non-native peptide derived from corticotropin-releasing factor-2, useful for treatment and prevention of e.g. muscular atrophy, also related nucleic acid and antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.3%; Score 19; DB 7; Length 5; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 394; 300pp; English.
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                                    16-JAN-2002; 2002US-0349117P.
29-APR-2002; 2002US-0376337P.
14-JUN-2002; 2002US-0388895P.
19-SEP-2002; 2002US-0411988P.
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16-JAN-2003; 2003WO-US001451
                                                                                                                                       (PROC ) PROCTER & GAMBLE CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                               Isfort RJ, Mazur WA;
                                                                                                                                                                                                                     WPI; 2003-787974/74.
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1 TKFTL 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5 AA;
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Activating sequence, Gal4, transcriptional activator, RNA polymerase, Protein-protein interaction, gene therapy, therapeutic, holoenzyme,
                                                                                                                                                                                                                                                                                   New transcriptional activator containing DNA binding domain bound to peptide - useful for controlling gene expression, especially in gene therapy, and in protein-protein interaction assays, does not inhibit other transcription activators.
                                                                   Transcriptional activator peptide fragment LS130.
                                                                                                                                                                                                                                                                                                                               Example 1; Page 26; 55pp; English.
                 AAW31467 standard; protein; 6 AA.
                                                                                                                                                                             97WO-US007338
                                                                                                                                                                                             96US-0017016P
                                                  04-AUG-1998 (first entry)
                                                                                               Protein-protein interactic
Gall1; DNA binding domain.
                                                                                                                                                                                                                                         Lu X, Wu Y;
                                                                                                                                                                                                                      (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                         WPI; 1998-018502/02.
N-PSDB; AAV02565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6 AA;
                                                                                                                                                                            02-MAY-1997;
                                                                                                                                         WO9744447-A2
                                                                                                                                                                                             03-MAY-1996;
01-MAY-1997;
                                                                                                                                                          27-NOV-1997
                                                                                                                                                                                                                                        Ptashne M,
                                                                                                                        Synthetic.
                                  AAW31467;
RESULT 9
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fragments used in an assay to determine novel transcriptional activators.

fragments used in an assay to determine novel transcriptional activators.

The method involves the production of transcriptional activators

comprising of a DNA-binding group and a 6-25 amino acid peptide that is

covalently bonded to the DNA binding group and does not represent a

fragment of a natural transcription activator. Protein-protein

interactions are identified in the assay by fusing a DNA-binding domain

to a library of DNA fragments and introducing this and a fusion of target

protein and a polypeptide containing a region of Gal4 which interacts

contein and a polypeptide containing GallIP and identifying members of the

protein and a polypeptide containing GallIP and identifying members of the

controlling gene activity, particularly in gene therapy (e.g. recognizing

a site close to a selected therapeutic gene). Transcription can be

activated without blocking other transcriptional activators. They

probably act by interacting with a component of the RNA polymerase II

holoenzyme, GallI, the strongest known yeast activator, which provides a

more sensitive assay allowing detection of even weak protein-protein

coverexpressed
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57.1%; Score 20; DB 2; Length 6;
80.0%; Pred. No. 1.4e+06;
ive 0; Mismatches 1; Indels
Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Specific example of pentapeptide of the general formula of AAP82197. These peptides can be administered intravenously, topically or perorally to relieve the symptoms of psoriasis or schizophrenia. Amino acids at posns 2 and 3 can be any residue but Asp is preferred at posn 3. See also AAP82196-9
                                                                                                                                                                                                                                                                                                                                        Short peptide(s) for treatment of psoriasis and schizophrenia - comprise vaso-active intestinal polypeptide, peptide T or short peptide with five aminoacid(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            corticotropin-releasing factor-2; CRF2; myopathic; osteopathic; hypotensive; cardiant; vasotropic; antimigraine; cerebroprotective; nootropic; neuroprotective; anorectic; antidiabetic; analgesic; antiallergic; tranquilizer; anxiolytic; antidepressant; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                     Example of peptide 2 for treatment of schizophrenia or psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                             schizophrenia; psoriasis; vasoactive intestinal polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corticotropin-releasing factor-2 polypeptide, SEQ ID No 394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 75.0%; Pred. No. 1.4e+06; 3; Conservative 1; Mismatches 0; Indels
             AAP82200 standard; protein; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE65091 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1, Page 5; 9pp; Swedish.
                                                                                                                                                                                                                87SE-00000125.
                                                                                                                                                                                                                                         87SE-00000125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                  WPI; 1988-328337/46.
                                                                                                                                                                                                                                                                (WETT/) WETTERBERG.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
                                                                                                                                                                                                                                                                                          Wetterberg L;
                                                              25-OCT-1990
                                                                                                                                                                                                                15-JAN-1987;
                                                                                                                                                                                                                                         15-JAN-1987;
                                                                                                                                                              SE8700125-A.
                                                                                                                                                                                       16-JUL-1988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy
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                                                                                                                                      Synthetic.
                                      AAP82200;
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Matches
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This sequence corresponds to a peptide (CDR-H1-7; AAY14403) derived from the sequence of the heavy chain variable region complementarity determining region (CDR)-1 of the anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (MAb) 8D4 protein. The peptide has a Tyr to Phe amino acid substitution at position 3 compared to the CDR-H1-7 peptide. The invention relates to the use of partial peptides (AAY14348-Y14353) from the MAb 8D4 for inhibiting HCV serine protease activity
                      Desmet J, Hufton S, Hoogenboom H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 24; 32pp; Japanese.
       (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                                                                  AAY14399;
                                                                                                                                                                               Query Match
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Matches
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Sequence 7 AA;

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Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neutralized antibody partial peptide derived from hepatitis C virus -
useful for inhibiting Hepatitis C Virus (HCV) serine protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complementarity determining region; CDR; monoclonal antibody; MAb; hepatitis C virus; HCV; protease; binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 74.3%; Score 26; DB 3; Length 7; Local Similarity 83.3%; Pred. No. 1.4e+06; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                   Disclosure; Page 15; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY14399 standard; peptide; 7 AA.
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WPI; 2000-665002/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
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The invention relates to diagnosing the presence of colon cancer, metastases of colon cancer, staging colon cancer, monitoring colon cancer for the onset of metastasis or monitoring a change in stage of colon cancer in a patient. The method involves determining a colon specific gene (CSG) in cells, tissues or bodily fluids and comparing it with levels of CSG in cells, tissues or bodily fluids from a normal human control. Colon cancer can be treated by administering a molecule which down regulates the expression or activity of CSG. An immune response against a target cell expressing CSG can be induced by delivering an immunologically stimulatory amount of a CSG protein to a patient, so that in immune response is mounted. Therapeutic agents are useful for imaging colon cancer in a patient by administering an agent labelled with for paramagnetic ions or a radioisotope to the patient. They are also useful for preventing the onset of colon cancer, and in diagnosis and treatment of the disease. Sequences AAU85424-AAU85502 represent human colon specific protein antibody binding sites used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing, staging or monitoring colon cancer involves determining colon specific gene in cells, tissues or body fluids in patient, and comparing it with levels of the gene from a normal human control.
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O
                                                                                                                                                                                                                                                                                                  Human colon specific polypeptide antibody binding site #31.
                                          i, Indels
              Length 7;
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                                                                                                                                                                                                                                                                                                                                  Human; colon specific gene, CSG; cytostatic; metastasis; colon cancer staging; antibody binding site.
        Score 21; DB 2; I
Pred. No. 1.4e+06;
0; Mismatches 1;
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60.0%; Scc...
80.0%; Pred
                                                                                                                                                                                              AAU85454 standard; peptide; 5 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-2000; 2000US-00618596
                                                                                                                                                                                                                                                                 (first entry)
        Query Match
Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DIAD-) DIADEXUS INC.
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                                                                          1 TOFTL 5
                                                                                                           TDEVL 5
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                21-MAY-2002
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                                                                                                                                                                                                                              AAU85454;
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Hoogenboom H,

(INNO-) INNOGENETICS NV. Desmet J, Hufton S,

98EP-00870065

31-MAR-1998;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.
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                                                                                                                                                                                                                                                                           Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosqlerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.1%; Score 27; DB 3; Length 7; 83.3%; Pred. No. 1.4e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                  Scaffold protein SCA S4 peptide SEQ ID NO: 136
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                            AAB30075 standard; peptide; 7 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-EP002283
                                                                                                                                                      (first entry)
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nes 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                          AAB30075;
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ID AAY4
XX
AC AAY4
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DT 01-D
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DE S4 d
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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta crands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands C functionally equivalent derivative of these sequences. The beta strands C functional beta strands A1-A3 are included in the structure the constructed of two beta sheets, with the structure the scaffold is constructed of two beta sheets, with the structures C scaffold is constructed of two beta sheets, with the structure of the scaffold is constructed of two beta sheets, with the structure of the receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold cor whole protein which hinds to a tumour antigen. This will the target the complex to tumour cells. Therefore the scaffold protein may be bound to a protein which hinds to a tumour antigen. This will the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                             New scaffold protein, useful for stabilizing antigens used as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.3%; Score 26; DB 2; 83.3%; Pred. No. 1.4e+06; ive 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scaffold protein SCA S4 peptide SEQ ID NO: 135.
                                                                                                                                                                                                                                    Disclosure; Page 6; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB30074 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3.
                                                                                                                                                       WPI; 1999-542958/46.
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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
                                                                                                                                                                                                                  85.7%; Score 30; DB 2; Length 7; 100.0%; Pred. No. 1.4e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scaffold protein SCA S4 peptide SEQ ID NO: 137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desmet J, Hufton S, Hoogenboom H,
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAB30076 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-EP002283
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Matches
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Sequences AANY 0607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta trands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands for the next by hydrogen bonds, which generate a beta sandwich architecture. C form two beta sheets S1/S4/S3 and S6/S5/S2 with each structures the scaffold is constructed of two beta sheets, with the structures to cother via amino acid loops, where at least one of the loops binds to a creceptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold cumplex to tumour cells. Therefore the scaffold protein may be used to target the complex to tumour cells. Another surface may be bound to a cyctoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences AAY40727-Y40748 are functionally equivalent derivatives of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New scaffold protein, useful for stabilizing antigens used as vaccines.
                                                                                                                                                                             Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.
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                                                                                                                                       S4 derivative #11, beta strand of scaffold protein structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 6; 105pp; English.
                AAY40737 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                    98EP-00870065.
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Best Local Similarity 83.33,
Ling 5, Conservative
                                                                                                 (first entry)
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                                                                                                 01-DEC-1999
                                                                                                                                                                                                                                                                               EP947582-A1.
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                                                         AAY40737;
AAY40737
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Query Match 85.7%; Score 30; DB 3; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 6; Conservative 0; Mismatches 0; Indels

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RESULT

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GenCore version 5.1/6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 1, 2004, 10:40:31; Search time 45.6667 Seconds (without alignments)
43.310 Million cell updates/sec

US-09-712-819C-5 35 1 TDFTLTI 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

92273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* .: geneseqp1980s:* : geneseqp1990s:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	ion	S4 deriva	Scaffold		SCA		Ø	Peptide C	Human col	Transcrip	Example o	Corticotr	CRF2 non-	Epitope t	Epitope t	AUS pepti	AUS pepti	Epitope t	Integrin	AUS epito	AUS pepti	Epitôpe t	AUS epito	Corticotr	CRF2 non-	Amaranthu
	Description	Aay40738	Aab30076	Aay40737	Aab30075	Aay40736	Aab30074	Aay14399	Aau85454	Aaw31467	Aap82200	Ade65091		φ	ø	Φ	o,	Aae13076	Aam51422	Aab97355	Aae24897	Abq32853	Add67264	Ade65099	Ade51385	Aay52584
	DI	AAY40738	AAB30076	AAY40737	AAB30075	AAY40736	AAB30074	AAY14399	AAU85454	AAW31467	AAP82200	ADE65091	ADE51377	AAY06466	AAE16558	AAY77708	AAB59859	AAE13076	AAM51422	AAB97355	AAE24897	ABG32853	ADD67264	ADE65099	ADE51385	AAY52584
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ALIGNMENTS

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent. 84 derivative #12, beta strand of scaffold protein structure. AAY40738 standard; peptide; 7 AA. 01-DEC-1999 (first entry) EP947582-A1. 06-OCT-1999. Synthetic. AAY40738; RESULT 1

98EP-00870065. 98EP-00870065. 31-MAR-1998; 31-MAR-1998;

(INNO-) INNOGENETICS NV.

Desmet J, Hufton S,

Hoogenboom H, Sablon E;

WPI; 1999-542958/46.

New scaffold protein, useful for stabilizing antigens used as vaccines.

Disclosure; Page 6; 105pp; English.

Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 5 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands C form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens

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                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Sperm attracting peptide SepSAP.
Sepia officinalis (Common cuttlefish).
Eukaryota, Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepia.
"A novel active pentapeptide from chicken brain identified by antibodies to FMRFamide.";

Nature 305:328-330(1983).

-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.

GO, GO:0007218; P:neuropeptide signaling pathway; TAS.

Neuropeptide; Amidation.

MOD RES

S AMIDATION.

SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;
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PubMed=12207899;
Zatylny C., Marvin L., Gagnon J., Henry J.;
Zatylny C., marvin L., Gagnon J., Henry J.;
"Fertilization in Sepia officinalis: the first mollusk spermatracting peptide.";
attracting peptide.";
Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
                                                                                                                                                                                                                   Query Match
17.1%; Score 6; DB 13; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 1; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AA; 597 MW; 72C8676AA0470000 CRC64;
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SEQUENCE

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Query Match

Best Loc Matches

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RESULT 11 Q47029

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"Characterization of the cmcH genes of Nocardia lactamdurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis."; Gene 162:21-27(1995).

EMBL, Z21682; CAA79797.1; -.
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
        Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
PubMed=6137771;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=8612033; PubMed=3003688; Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.; Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.; Spinach plastid genes coding for initiation factor IF-1, ribosomal protein S11 and RNA polymerase alpha-subunit."; Nucleic Acids Res. 14:1029-1044(1986). EMBL; X03496; CAA27215.1; -. GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytochrome b/f subunit IV (Fragment).
Spinacia oleracea (Spinach).
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.
NCBI TaxID=3562;
                                                                                                                                                                                                                                                                                                                                0; Indels
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Last annotation update)
(LPLRF-amide).
                                                                                                                                                                                                                      7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
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                                                                                                                                                                                                                                                                          20.0%; Score 7; DB 2;
50.0%; Pred. No. 1e+06;
tive 1; Mismatches
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vative 1; Mismatches
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01-JUN-2002 (TrEMBLrel. 21, Cr
01-JUN-2002 (TrEMBLrel. 21, La
01-JUN-2003 (TrEMBLrel. 24, La
FMRFamide-like neuropeptide (L
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 1; Conservative
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Liras P.;
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SEQUENCE
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MEDLINE=94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.,
"Analysis of the aac(3)-VIa gene encoding a novel 3-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
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Enterobacteriaceae, Enterobacter.
NCBI_TaxID=550,
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Pseudonocardineae, Pseudonocardiaceae, Amycolatopsis.
NCBI_TaxID=1913;
                                                                                                                                                                                                                                                                                                                                                                                                            Match 20.0%; Score 7; DB 2; Length 5; Local Similarity 50.0%; Pred. No. 1e+06; es 1; Conservative 1; Mismatches 0; Indels
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                                                                                  89 kDa protein (Fragment).
Bacillus cereus.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acetyltransferase.";
Antimicrob. Agents Chemother. 37:2074-2079(1993)
EMBL; M88012; AAA16193.1; -.
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01-FEB-1997 (TrEMBLrel. 02, Last sequenc
01-DEC-2001 (TrEMBLrel. 19, Last annotat
3'-methylcephem hydroxylase (Fragment).
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SEQUENCE FROM N.A.
MEDLINE=96009872; PubMed=7557411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aad Al protein (Fragment)
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Matches 1; Conserv
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STRAIN=E;
MEDLINE=96427318; PubMed=8830682;
Rehm B.H.A., Ertesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algg) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL; X87973; CAA61230.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
NCBI_TaxID=354;
                                                                                                                                                                                                                                                                         STRAIN=DSM 20451;
PubMed=1212860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Drews O., Weiss w., Reil G., Parlar H., Wait R., Goerg A.;
"High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
               P83533;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 22.9%; Score 8; DB 2; Length 6; Local Similarity 50.0%; Pred. No. 1e+06; nes 1; Conservative 1; Mismatches 0; Indele
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
AlgT protein (Fragment).
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SEQUENCE 7 AA; 684 MW; 71B5A5A5D1AED0 CRC64;
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Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches
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PRELIMINARY;
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P83073;
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                                                                                 01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10 kDa cell wall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Nicotiana.
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STRAIN=4874;
MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002);
EMBL; AF347267; AAK32344.1; -.
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Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
"Proteomic study of secondary cell wall proteins from transformed
tobacco culture.";
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1e+06;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER 7 7 7 SEQUENCE 7; AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOW 15K 1 SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
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Best Local Similarity 33.3%; Pred. No. 1e+0
Matches 1; Conservative 2; Mismatches
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-!- TISSUE SPECIFICITY: XYLEM.
GO; GO:0005618; C:cell wall; IEA.
                                           PRT;
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Best Local Similarity
Matches 2; Conserv
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STRAIN=RF-1;
MEDLINE=99231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
Gabs
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Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sphingomonas chungbukensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
NCBI_TaxID=56193;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim Y.-C.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 25.7%; Score 9; DB 2; Length 7; Local Similarity 66.7%; Pred. No. 1e+06; les 2; Conservative 0; Mismatches 1; Indels
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nifk (Fragment).
                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Catechol-2,3-dioxygenase (Fragment).
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SEQUENCE 7 AA, 868 MW, 71A452D1A699D460 CRC64;
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1; Mismatches
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EMBL; AF003700; AAC35193.1; -.
  2; Conservative
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STRAIN=N2-3-11;
MEDLINE=20011291; PubMed=10542330;
MEDLINE=20011291; PubMed=10542330;
Poehling S., Piepersberg W., Wehmeier U.F.;
"Analysis and regulation of the sec Y gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";
Blochim. Blophys. Acta 1447:298-302(1999).
EMBL; X95915; CAA65160.1; -.
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PubMed=12112860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
"High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774 (2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces griseus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1911;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
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Pred. No. 1e+06;
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Query Match

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Q54248 streptomyce
P83530 lactobacill
O34028 sphingomona
O07354 synechococc
P82445 nicotiana t
Q8je81 human immun
P83533 lactobacill
P70804 azotobacter
P83073 bacillus ce
Q47029 enterobacte
P72081 nocardia al
O98866 spinacia ol
P83308 gallus gall
P83569 sepia offic
P82541 spinacia ol
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GenCore version 5.1/6
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"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043704; AAO38592.1; ".
Hypothetical protein.
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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ID ALL5 CARMA STANDARD; PRT; 7 AA.

AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidea; Portunidae; Carcinus.

ON NCBI TaxID=6759;
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Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;
"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
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MEDLINE=98121193, Pubmed=9461295,
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Bubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI_TaxID=6759;
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ALL4 CARMA
ID ALL4 CARMA
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allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD RES
7 7 AMIDATION.
SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;
                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                    22.9%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; ative 0; Mismatches 1; Indels
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Best Local Similarity
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Local Similarity
les 2; Conserv
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P81805;
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P81806;
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ALL3 CARMA
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Phytogulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
TISSUE=Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wallace J.C.;
Tyler M.J., Wallace J.C.;
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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-!- PTM: Sulfation is important for activity and for the binding to putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
STRAIN=cv. US-Harumakigosun;
MEDLINE=20212743; PubMed=10750705;
Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
Kamada H., Sakagami Y.;
"A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";
Plant Cell Physiol. 41:27-32(2000).
-!- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
cells, but does not stimulate differentiation into the somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 2.1.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò.
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3 3 SULFATION.
5 AA, 687 MW, 76C1BBS04B300000 CRC64;
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RE21 LITRU
STANDARD; PRT; 5 AA.
AC P82071;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloide
OC Pelodryadinae; Litoria.
OX NCBI TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUES AND MASS SPECTROMETRY.
RA TYLER M.J., Wallace J.C.;
RA TYLER M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian and th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHYTOSULFOKINE-BETA
                                                                                                                                                                                                                                                                                 5 AA
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                                                                                                                                                                                                                                                                                    PRT;
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Local Similarity 50.0%;
nes 1; Conservative
                                                                                                                                                                                                                                                                                 STANDARD;
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MOD RES
MOD RES
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PSK DAUCA
ID PSK D
AC PS826
DT 16-0C
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Matches
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-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thorpe A.;
"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD_RES 7 7 7 AMIDATION (POTENTIAL).
SEQUENCE 7 AA; 770 MW; 672879CDE5DDB70 CRC64;
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MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                            activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=626; METHOD=FAB.
Amphibian defense peptide.
SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.
                                                                                                                                                                                                                                             Query Match 22.9%; Score 8; DB 1; Length 5; Best Local Similarity 50.0%; Pred. No. 1.4e+05; Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Cerebral ganglion, and Thoracic ganglion; MEDLINE=98121193; PubMed=9461295;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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EI04 LITRU ID EI04 LITRU AC P82100;

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SEQUENCE.
MEDIJNE=87005252; PubMed=3093276;
MOLI M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INOUPE A.;
"Isolation and identification of multiple neuropeptides of the misolation and identification of multiple neuropeptides of the malatostatin superfamily in the shore crab Carcinus maenas.";

Bur. J. Biochem. 250:727-734(1997)

-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation; Multigene family.

MOD_RES
5 AMIDATION (POTENTIAL).

SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
NCBI TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          caM373.";
FEBS Lett. 206:69-72(1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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22.9%; Score 8; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.7%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; rative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL14 CARMA STANDARD; PRT; 5 AA. P81817; 5 AA. 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                             PRT;
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2; Conserv
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Best Local S
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AL14_CARMA
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cCF10.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89008313; PubMed=3139658;
Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Adsit J.C., Dunny G.M., Suzuki A.;
"Structure of cCF10, a peptide sex pheromone which induces
conjugative transfer of the Streptococcus faecalis tetracycline
resistance plasmid, pCF10.";
J. Biol. Chem. 263:14574-14578 (1988).
-; FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PCF10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin secretion; Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                               Litoria rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
NCBI TaxID=104895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
28.6%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
MOD RES 5 5 AMIDATION.
SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                 S AA.
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Best Local Similarity 100.0
Matches 2; Conservative
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CCF1 ENTFA

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SEQUENCE

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TISSUE-Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
Amphibian defense peptide; Amidation.
MOD_RES 5 5 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    Litoria rubella (Desert tree frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                         Rubellidin 3.1
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                                                                         RESULT 4

RE31_LITRU

DC RE31_LITRU

AC P82072;
DT 28-FEB-2003
DT 10-OCT-2003
DE Rubellidin 3
OC Amphibia; Ba
OC Amphibia; Ba
OC Pelodryadina
OX NCBI_TAXID=1
RN [1]
RP SEQUENCE, AN
RC TISSUE-Skin
RA TYler M.J.,
RT 'Litoria rube
CC TISSUE-Skin
RT 'Litoria cut
RT 'Litoria
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EMBL; M21922; -; NOT_ANNOTATED_CDS.
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MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
"Iranscriptional regulation and Salmonella typhimurium biotin operons.";
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(BC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                      activity.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
Amphibian defense peptide.
SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         Query Match 34.3%; Score 12; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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PROSITE; PS00600; AA TRANSFER CLASS 3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
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31.4%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels

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Gaps
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                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
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-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

Amphibian defense peptide.

Amphibian defense peptide.

AROUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.4%; Score 11; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                s AA.
                                                    STANDARD;
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RE32_LITRU
AC P82073;
DT 28-FEB-2003
DT 28-FEB-2003
DT 10-OCT-2003
DE Rubellidin 3
OS Litoria rube
OC Amphibia; Ba
CT ISSUE=Skin
RA Wabnitz P.A.
RT "Peptides fi
RT "Peptides fi
RT Litori elect
RT RT LITORI elect
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GenCore version 5.1.6
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- protein search, using sw model OM protein June 1, 2004, 10:41:50; Search time 7.66667 Seconds (without alignments) 47.542 Million cell updates/sec Run on:

US-09-712-819C-5 35 1 TDFTLTI 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P82158 cvdia pomon	litori	-		P82073 litoria rub		_						P81806 carcinus ma		P81808 carcinus ma	P31889 ascaris suu	36515	moniezi		clostri									P35904 achatina fu	P42562 hirudo medi	263	58705 anthopl	_
SUMMARIES	ALL7 CYDPO	RE11_LITRU	BIOA_CITFR	RE31_LITRU	RE32_LITRU	EI04_LITRU	CCF1_ENTFA	CIA ENTFA		PSK_DAUCA	RE21_LITRU	ALL2_CARMA	ALL3_CARMA	ALL4_CARMA	ALLS_CARMA	FAR1_ASCSU	RM01_YEAST	FARP_MONEX	LOK1_LOCMI	UNOG_CLOPA	FAR1_MACRS	FAR1_PROCL	FAR2_PROCL	FAR4_PANRE	FARB_CALVO		IGAO_DACDE		ACH1_ACHFU	FAR3_HIRME		FFKA_ANTEL	FLRF_HIRME
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TISSUE=Skin secretion,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.,
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";

SEQUENCE, AND MASS SPECTROMETRY.

REII LITRU STANDARD; PRT; 5 AA.
P82070;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 1.1.
Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.

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	STANDARD	39, 39, 39, 39, 39, 19, 12, 12, 12, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13	rvat
	ST	(Rel.	Similarity 3; Conser
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	T 1 CYDPO ALL7 C	982158; 30-MAY-200 30-MAY-200 30-MAY-200 30-MAY-200 Cydiastati Cydiastati Cydiastati Cydiastati Cydiastati Neoptera; Tortricoic NCB TaxII SEQUENCE. TSSUE-La MEDLINE-98 Duve H., J Davey M., "Lepidopte Peptides 1 Peptides 1 Neurospti MOD RES SEQUENCE	78 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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	RESULT ALL7_C ID_A	STANGE REPRESENTATION STANGED TO THE STANGE REPRESENTATION OF THE STANGE R	ű űc

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C;Accession: A60986
R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methiony A;Reference number: A60986; MUID:90092408; PMID:2689204
A;Accession: A60986
A;Molecule type: protein
A;Residues: 1-6 <BRO>
C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.
F;1/Modified site: N-formylmethionine #status experimental
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Species: Escherichia coli
Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
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A;Reference number: S69237; MUID:95139068; PMID:7837271
A;Accession: S69237
A;Molecule type: protein
A;Residues: 1-5 <PET>
A;Experimental source: strain F1, DSM 3639
C;Keywords: cell wall; glycoprotein; heat-stable protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 1, 2004, 11:19:23 Job time: 11.6667 secs
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C;Species: Staphylothermus marinus
C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
R;Peters, J.; Nitsch, M.; Kuehlmorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; E
J. Mol. Biol. 245, 385-401, 1995
A;Title: Tetrabrachion: a filamentous archaebacterial surface protein assembly of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diood cell protein B - Ascidia ceratodes (fragment)
N;Alternate names: Abcp-B
C;Species: Ascidia ceratodes
C;Species: Ascidia ceratodes
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jun-1999
C;Accession: S68326
R;Taylor, S.W.; Ross, M.M.; Waite, J.H.
Arch. Biochem. Biochys. 324, 228-240, 1995
A;Fitle: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides fr
A;Reference number: S68325
A;Reference number: S68326
A;Molecule type: protein
A;Residues: 1-5 <TAY>
F;2/Modified site: 3',4',5'-trihydroxyphenylalanine (Tyr) #status experimental
F;4/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the A;Reference number: A60274; MUID:91099989; PMID:1898899
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Best Local Similarity 100.0%; Pred. No. 2.6
Matches 2; Conservative 0; Mismatches
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     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <VOG>
A;Cross-references: GB:M62408
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A,Molecule type: protein
A,Residues: 1-5 <NAG>
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T13892
cytochrome—c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (frag cytochrome—c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey)
C;Specimitochondrion Lampetra fluviatilis (river lamprey)
C;Spate: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Biol. Baviel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Reference number: Z17775; MUID:97398704; PMID:9254918
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Residuse: 1-3 <DEL>
A;Molecule type: DNA
A;Residuse: 1-3 <DEL>
A;Genome: mitochondrion
A;Molecule coll
C;Keywords: mitochondrion; oxidoreductase
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C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: E42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J; Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq A;Reference number: A42364; MUID:91258342; PMID:1646201
                                                                                                                                                                                                                                                                                                                           Globulin IV alpha subunit delta-1 chain, seed - cucurbit (fragments)

globulin alpha subunit delta-1 chain

C; Alternate names: 11S globulin alpha subunit delta-1 chain

C; Species: Cucurbita sp. (cucurbit)

C; Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996

C; Accession: S09066

R; Ohmiya, M.; Hara, I.; Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980

A; Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and A; Reference number: S09066

A; Rccession: S09066

A; Molecule type: protein

A; Residues: 1-6;7 < OHM>
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Query Match 28.6%; Score 10; DB 2; Length Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 1; Inde
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biotin A - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Accession: 140697
C;Citranscriptional regulation and gene arrangement of Escherichia coli, Citralscriptional regulation and gene arrangement of A;Reference number: 140697
C;Accession: 140697
C;Citranscriptional regulated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4 <- RES>
C;Accession: A;Residues: 1-4 <- RES>
C;Citranscriptional regulation and Gene arrangement of Escherichia coli, Citralscriptional regulation and Gene arrangement of Escherichia coli, Citralscription and Gene arrangement of Escherich
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0650
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 16-Aug-1996
C;Accession: E30608
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM A;Reference number: A30601; MUID:89215279; PMID:2496160
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
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31.4%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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C;Species: Homo sapiens (man)
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A;Residues: 1-7 <GON>
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 40.0
Matches 2; Conservative
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J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601; PMID:1711558
A; Accession: PT0665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C;Accession: B39127
R;Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A;Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of
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T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0644
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T-cell receptor beta chain V-D-J region (121-3BM) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C; Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.3%; Score 12; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5;
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A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Reference number: A39127; MUID:91100329; PMID:1846143
A,Accession: B39127
A,Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.3%; Score 12; DB 2; L
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1;
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2 SSFT 5
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 1, 2004, 10:56:46; Search time 11.6667 Seconds (without alignments) 57.715 Million cell updates/sec Run on:

US-09-712-819C-5 35 1 TDFTLTI 7 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

457 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 st

summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d			SUMMARLES	
Result No.	Score	Query Match	Length	DB	ΩI	Description
! "				! (1 6	
-	T	7 . 7	٥	V	200	pev-kının 2 - pena
7	12	34.3	ហ	N	A32516	cholecystokinin-5
ო	12	34.3	ហ	a	PT0644	T-cell receptor be
4	12	34.3	7	N		phosphotransferase
Ŋ	12	34.3	7	7		
Q	11	31.4	4	7		biotin A - Citroba
7	11	31.4	7	7	E30608	
œ	10	28.6	ø	C)		T-cell receptor be
σ	10	ω.	7	~		IV alph
10	თ	25.7	m	m		cytochrome-c oxida
11	on	25.7	Ŋ	α		flagellar protein
12	ወ	25.7	Ŋ	N	E60274	orot
13	σı	25.7	ß	N	568326	blood cell protein
14	σ	25.7	ω	7	869237	surface protein te
15	Q	25.7	v	N	A60986	м
16	O)	25.7	G	~	B44510	hypothetical prote
17	თ	25.7	9	7	A43766	28K ubiquitin-immu
18		25.7	w	N	I37263	Y protein - human
19	0	'n.	v	N	I65546	HC H2-1
20	6	25.7	vo	Ŋ	PT0587	T-cell receptor be
21	<u>ი</u>	'n	φ	Ŋ	S29881	Na+/K+-exchanging
22	σı	N	7	Ŋ	825266	pilE protein - Esc
23	თ	ъ.	7	N	A25269	heromone c
24	σı	25.7	7	~	A30812	sex pheromone cCF1
25	σ	'n	7	N	PT0611	-cell recepto
56	80	ď	4,	N	PT0697	cell
27	8	ď.	ß	Ŋ	I39964	mal protei
28	œ	22.9	S	N	I39966	ribosomal protein
29	œ	٥.	Ŋ	Ŋ	966	_

5 2 A44692 5 2 PT0590 5 2 PT0590 5 2 E44817 5 2 E44817 5 2 C44817 5 2 A44817 6 2 A44817 6 2 A19780 6 2 PT0641 7 2 E61491 7 2 PS0254 7 2 PT0642	fulicin - giant Af T-cell receptor be T-cell receptor be	7.5 kda structu 7.5K structural 7.5K structural	28.5K structural p 28K structural pro phytosulfokine alp	errin ilon I receg	T-cell receptor be seed protein ws-5 18K protein 5507 -	T-cell receptor be
,	10 10	G44817 I44817 E44817	C44817 A44817 JT0870	A19780 A46474 PT0637	PT0641 E61491 PS0254	PT0642
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	0 H 8	። ተ ። የ ተ ።	33 34 34 34	3.9 4.4 1.0 1.0	4 4 4 4 4 4	45

ALIGNMENTS

RESULT 1 PD0028	pev-kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment) C;Species: Penaeus vannamei	C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000 C;Accession: PD0028	R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devr Biochem, Biophys, Res. Commun. 248, 406-411, 1998	A; Title: Identification of one tachykinin- and two kinin-related peptides in the br	A;Reference number: PD0027; MUID:98342103; PMID:9675150	A;Accession: PD0028	A, Molecule type: protein	A; kesiques: 1-6 ANIES	Cicomment: This peptide belongs to myotropic neuropeptides.	Query Match 37.1%; Score 13; DB 2; Length 6;	at Similaricy 66./*; Fred. No. 2.8e+05;	Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Oy 2 DFT 4	Db 1 DFS 3
						_		_						

Chochestokinin-5 - dog
NiAlternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Reference number: A32516
A;Residues: 1-5 <SHI>C;Comment: This peptide corresponds to the five carboxyl-terminal residues of chole C;Superfamily: gastrin
C;Superfamily: gastrin
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; Neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

. 0 Query Match 34.3%; Score 12; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

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Gaps

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Gaps

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RESULT 15
US-08-386-653-46
; Sequence 46, Application US/08388653
; Patent No. 5869337
; GENERAL INFORMATION:
; APPLICANT: Crabtree, Gerald R.
; APPLICANT: Spencer, David M.
; APPLICANT: Spencer, David M.
; APPLICANT: Belshaw, Peter
TITLE OF INVENTION: REGULATED TRANSCRIPTION OF TARGETED
; TITLE OF INVENTION: GENES AND OTHER BIOLOGICAL EVENTS
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARIAD Pharmaceuticals, Inc.
; STREET: 26 Landsdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
                                                                Score 16; DB 2; Length 6; Pred. No. 3e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 16; DB 2; Length 6; 75.0%; Pred. No. 3e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIF: 02139
ZIF: 02139
ZIF: 02139
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,653
FILING DATE: 14-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,386
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 27,195
TELECOMMUNICATION INFORMATION:
MEDICALION INFORMATION:
MEDICALION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 27,195
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Job time: 14.6667 secs
                                                              Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 46
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0
Best Local Similarity 75.0
Matches 3; Conservative
         ; MOLECULE TYPE: protein US-08-292-597-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-388-653-46
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Pred. No. 3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC/DOS/MS/DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,386A
FILING DATE: 07/JUN/1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 2054-114A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Figg, E. Anthony
REGISTRATION NUMBER: 27,195
REFERENCE/DOCKET NUMBER: 2054
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6040
TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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TOPOLOGY: linear
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Gaps

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US-08-252-995D-7
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APPLICANT: Barberger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER PILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                      APPLICANT: Sandle, Inger
APPLICANT: Sandle, Inger
APPLICANT: Bogen, Bjarne
APPLICANT: Bogen, Bjarne
APPLICANT: Fossum, Sigbjorn
IITLE OF INVENTION: A Modified Immunoglobulin Molecule
IITLE OF INVENTION: Incorporating an Antigen in a No. 6294654-CDR
IITLE OF INVENTION: Loop Region
IITLE OF INVENTION: Loop Region
FILE REFERENCE: 9914-1
CURRENT APPLICATION NUMBER: US/08/860,904
CURRENT FILING DATE: 1997-09-29
EARLIER FILING DATE: 1996-01-19
EARLIER APPLICATION NUMBER: GB 9501079.9
EARLIER FILING DATE: 1995-01-19
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47, Application US/09301593A Patent No. 6455677 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-252-995D-7
; Sequence 7, Application US/08252995D
US-08-860-904-9; Sequence 9, Application US/08860904; Patent No. 6294654; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-301-593-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus sp.
US-08-860-904-9
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PRESENT NO. SESSORY

PRESENT NO. SESSORY

PRESENT NO. SESSORY

PAPLICANT: BEGGETAIN, MIKE

APPLICANT: BEGGETAIN, MIKE

APPLICANT: BEGGETAIN

PROSESSER: PRESENTE FROM

CORRESPONDERS A. DERESSI.

ADDRESSER: PROPERTY

COMPATING STREET: PROPENTY

COMPATING S
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Milwaukee
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US-08-753-750B-19
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APPLICANT: Unilever PLC
TITLE OF INVENTION: New products comprising inactivated yeasts or moulds
TITLE OF INVENTION: provided with active antibodies
FILE REFERENCE: t-7055
CURRENT APPLICATION NUMBER: US/09/266,805
CURRENT FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                            Gaps
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US-09-530-139-14
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US-09-530-139-14

Sequence 14, Application US/09530139

Patent No. 6670453

GENERAL INFORMATION:

APPLICANT: FRENKEN, LEON GERARDUS

APPLICANT: LEDEBOER, ADRIANUS MARINUS

APPLICANT: LEDEBOER, ADRIANUS MARINUS

APPLICANT: VAN DER LOGT, CORNELIS PAUL

TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS

FILE REFERENCE: 60113/268075/ASH

CURRENT APPLICATION NUMBER: DC7/EP98/06991

PRIOR APPLICATION NUMBER: PC7/EP98/06991

PRIOR FILING DATE: 1998-10-27

PRIOR FILING DATE: 1998-10-27

MUMBER OF SEQ ID NOS: 77

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 14
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Patent No. 5837461
GENERAL INFORMATION:
APPLICANT: Neitz, Maureen E.
APPLICANT: Neitz, John F.
TITLE OF INVENTION: DETECTION OF CONE-PHOTORECEPTOR-BASED TITLE OF INVENTION: VISION DISORDERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 411 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                             53.1%; Score 17; DB 4; Length 6; 60.0%; Pred. No. 3e+05; 1ive 2; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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; ORGANISM: llama
US-09-266-805-5
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PAPLICANT: Lo, Reggie Y.C.

APPLICANT: Lo, Reggie Y.C.

APPLICANT: Schryvers, Anthony B.

APPLICANT: Schryvers, Anthony B.

TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF

TITLE OF INVENTION: PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME

FILE REFERENCE: A34762 021645.0105

CURRENT APPLICATION NUMBER: US/08/753,750B

CURRENT FILING DATE: 1996-11-29

PRIOR APPLICATION NUMBER: CA 2,164,274

PRIOR APPLICATION NUMBER: 60/008,569

PRIOR FILING DATE: 1995-12-01

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19

LENGTH: 7

LENGTH: 7

LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 2; Length 7; Pred. No. 3e+05; 0; Indels 1; Mismatches
STATE: Misconsin
COUNTRY: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/739,401A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baker. Jean C.
REGISTRATION NUMBER: 650053.91151
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (414) 277-5709
TELEFAX: (414) 277-5709
TELEFAX: (414) 277-5709
TELEFAX: A140 277-5709
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75.0%;
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Best Local Similarity 33.3%;
Matches 2; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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APPLICANT: Boulanger, Pierre
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
APPLICANT: Hong, Saw See
TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses
FILE REFERENCE: 032751-036
CURRENT APPLICATION NUMBER: US/09/155,613A
CURRENT FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: FR 97/01005
PRIOR FILING DATE: 1997-01-30
PRIOR FILING DATE: 1997-01-30
PRIOR FILING DATE: 1997-01-30
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.1%; Score 17; DB 3; Length 5; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
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Pred. No. 3e+05;
1; Mismatches 0; Indels
           PatentIn Release #1.0, Version #1.25
                                                                                                                     ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6004.US.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847-935-1729

TELEFAX: 848-938-2623

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
SOFTWARE: PACELLL CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/09155613A Patent No. 6420120
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Best Local Similarity 75.0%;
Matches 3; Conservative
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; OTHER INFORMATION: Phagotope
US-09-155-613A-59
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Best Local Similarity
Matches 4; Conserv
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US-09-266-805-5
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LENGTH: 6
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Sequence 637, Application US/09839542B;
Patent No. 656996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: CADPOUNDS AND METHODS FOR MODULATING NONCLASSICAL TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                                 CTHER INFORMATION: Representative linear modulating agent based on CTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CTHER INFORMATION: recognition sequence US-09-187-859-637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Representative linear modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MUKERUI, PRADIP
APPLICANT: MUKERUI, PRADIP
APPLICANT: HARDS, ROBERT G.
APPLICANT: THURMOND, JENNIPER M.
APPLICANT: LEONARD, AMANDA EUN-YEONG
TITLE OF INVENTION: METHODS OF PRODUCING A RECOMBINANT PROTEIN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ohe Abbott Laboratories
STREET: Ohe Abbott Park Road
CITY: Abbott Park
STATE: Illinois
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                                                                                                                                                                                                  Query Match 56.2%; Score 18; DB 4; Length 7; Best Local Similarity 57.1%; Pred. No. 3e+05; Matches 4; Conservative 1; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/08757177 Patent No. 6071718 GENERAL INFORMATION:
             TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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US-09-839-542B-637
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US-08-757-177-16
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Sequence 20, Appl Sequence 637, App Sequence 16, Appl Sequence 16, Appl Sequence 14, Appl Sequence 16, Appl Sequence 16, Appl Sequence 17, Appl Sequence 46, Appl Sequence 55, Appl Sequence 55,
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                                                                                                                                                                                                               June 1, 2004, 11:13:51; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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1: /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-187-859-637
US-09-839-542B-637
US-08-757-177-16
US-09-155-613A-59
US-09-266-805-5
US-09-266-805-5
US-09-266-805-5
US-08-739-401A-6
US-08-739-401A-6
US-08-739-401A-6
US-08-739-401A-6
US-08-860-904-9
US-08-252-995D-7
US-08-252-995D-7
US-08-388-653-46
US-08-388-653-46
US-08-388-653-46
US-08-187-230-46
US-09-087-716-46
US-09-157-753-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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32
1 FTLTISS 7
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Match Length
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Perfect score:
Sequence:
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                                                                                                                                                                                                               Run on:
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No.
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Sequence 7, Appli Sequence 28, Appli Sequence 28, Appl Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl Sequence 24, Appl Sequence 26, Appl Sequence 62, Appl Sequence 41, Appl		ES CONTAINING THE SAME	.7; els 0; Gaps 0;		G NONCLASSICAL
ក ខាត្ឋប្រសិត្ត ក្រុងទិ «		INS OF AND VACCINES	4; Length 7 5; 1; Indel		FOR MODULATING
8-177-109A-7 8-687-706-7 9-040-216-28 8-136-743B-63 8-667-001-22 9-040-216-55 8-591-632-17 8-591-632-17 8-591-632-23 8-591-632-23 8-591-632-23 8-591-632-23 8-591-632-23 8-591-451-23 8-611-451-25 8-136-743B-62 8-297-731-4 8-290-448A-41 8-290-448A-41 8-220-448A-41	ALIGNMENTS	750B BINDING PROTEINS HAEMOLYTICA AND 05 8/753,750B 64,274 ;569 resion 4.0	20; DB No. 3e+0 smatches		RESULT 2 US-09-187-859-637 Sequence 637, Application US/09187859A Fatent No. 6358920 GENERAL INFORMATION: APPLICANT: Blaschuk, Orest W. APPLICANT: Gour, Barbara J. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODU TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS FILE REFERENCE: 100086.407C1 CURRENT APPLICATION NUMBER: US/09/187,859A CURRENT FILING DATE: 1998-11-06 NUMBER OF SEQ ID NOS: 4052 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 637 LENGTH: 7
	AL	nny B. RRIN BINI FELLA HAI 1-29 1-29 1-29 1-29 1-29 1-29 1-29 1-29	; Score ; Pred. 3; Mi		09187855 S AND ME -MEDIATE US/09/16
<i>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</i>		RESULT 1 US-08-753-750B-20 US-08-753-750B-20 Sequence 20, Application US/08753750B Patent No. 6610506 GENERAL INFORMATION: APPLICANT: Lo, Reggie Y.C. APPLICANT: Schryvers, Anthony B. APPLICANT: Potter, Andrew A. TITLE OF INVENTION: PASTEURELLA HAEMOL: TITLE OF INVENTION: PASTEURELLA HAEMOL: FILE REFERENCE: A34762 021645.0105 CURRENT APPLICATION NUMBER: US/08/753,7 CURRENT APPLICATION NUMBER: CA 2,164,274 PRIOR FILING DATE: 1995-11-01 PRIOR FILING DATE: 1995-12-01 PRIOR FILING DATE: 1995-12-01 PRIOR FILING DATE: 1995-12-01 NUMBER OF SEQ ID NOS: 68 SOFTWARE: FastSEQ for Windows Version 4 SEQ ID NO 20 LENGTH: 7 TYPE: PRT ORGANISM: Escherichia coli US-08-753-750B-20	62.5% y 42.9% rvative	7	ation US/ , Orest W rbara J. COMPOUND CADHERIN 086.407C1 NUMBER: 1998-11 S: 1998-11
N N N 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		Applicati Applicati 10506 NEMATION: Lo, Reggie Schryvers Potter, A VENTION: TUGNTION: TUG DATE: CATION NUM G DATE: EQ ID NOS: astSEQ for Escherichi	Similarity 3; Conser	TLTISS ::: TLSVDA	37 Applicable Service
9 9 9 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		HT 1 8-753-750B- quence 20, tent No. 66 heral INCORNEAL INCORNEAL TILE OF INV TILE OF TILE TILE OF INV TILE OF TILE TILE TILE OF TILE TILE TILE OF TILE TILE TILE TILE TILE TILE TILE TILE	Query Match Best Local Si Matches 3;	<u>й</u> —й	2 87-859-6 nnce 637, t. No. 63 ALANT: B ICANT: G E OF INV REFEREN REFEREN ENT APPL ENT APPL E
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 US-08-75 Sequent Patent APPLI APPLI TITLE TITLE TITLE PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR TYPE SEQ ID LENG TYPE	Query Best] Match	S d	RESULT Sequents Sequents Patents Patents Patents Papels Pa
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US-10-020-354-102
is Sequence 102, Application US/10020354
is Publication No. US20030190311A1
is GENERAL INFORMATION:
is APPLICANT: DALL'ACQUA, WILLIAM
APPLICANT: DALL'ACQUA, WILLIAM
APPLICANT: JOHNSON, LESLIE
is APPLICANT: WARD, ELIZABETH SALLY
ITTLE OF INVENTION: MOLECULES WITH EXTENDED HALF-LIVES, COMPOSITIONS AND USES THEREOF
FILE REFERENCE: 10271-027
CURRENT APPLICATION NUMBER: 00/254,884
is PRIOR FILING DATE: 2000-12-12
is PRIOR FILING DATE: 2000-12-12
is PRIOR FILING DATE: 2001-05-09
in NUMBER OF SEQ ID NOS: 118
is SOFTWARE: Patentin version 3.1
is SEQ ID NO 102
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                                                                                                                                                                                                                                           APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAPa-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890002
CURRENT APPLICATION NUMBER: US/10/159,006
CURRENT FILING DATE: 2002-06-03
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-29
PRIOR PILING DATE: 1999-04-30
PRIOR PILING DATE: 1998-04-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47
     Gaps
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     1; Indels
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0; Mismatches
                                                                                                                                                                                           Sequence 47, Application US/10159006
Publication No. US20030143229A1
4; Conservative
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Best Local Similarity 75.(
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-47
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ORGANISM: Homo sapiens
                                         3 LTISS 7
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1 TVSS 4
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Matches
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RESULT 12
US-10-156-820-59
i Sequence 59, Application US/10156820
i Publication No. US2020150558A1
i GENERAL INFORMATION:
i APPLICANT: BOULLANGER, Pierre
i APPLICANT: Hong, Saw See
i APPLICANT: Arayan, Lucie
i TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses;
FILE REFERENCE: 032751-036
i CURRENT APPLICATION NUMBER: US/10/156,820
CURRENT FILING DATE: 1998-01-30
i PRIOR FILING DATE: 1998-01-30
i PRIOR FILING DATE: 1997-01-30
i RUMBER OF SEQ ID NOS: 98
i SOFTWARE: FastSEQ for Windows Version 4.0
i EBNGTH: 6
i LENGTH: 6
Gaps
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APPLICANT: MUELLER, JOHN L.

APPLICANT: MUELLER, JOHN L.

APPLICANT: OZA, VIBHA B.

APPLICANT: PINDEIS, MARK A.

TITLE OF INVENTION: PEPTIDIC MODULATORS OF THE ANDROGEN RECEPTOR

FILE REFERENCE: PPI-110

CURRENT APPLICATION NUMBER: US/10/097,175

CURRENT PILING DATE: 2002-03-12

PRIOR PILING DATE: 2001-03-12

PRIOR PILING DATE: 2002-01-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 97

LENGTH. C.
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.1%; Score 17; DB 14;
80.0%; Pred. No. 1e+06;
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Pred. No. 1e+0
1; Mismatches
 Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Phagotope US-10-156-820-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 3; Conservative
4; Conservative
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Best Local Similarity
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Matches
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Publication No. US20040067523A1

GENERAL INFORMATION:

APPLICANT: MERKULOV, Gennady et al.

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL001103CON

CURRENT APPLICATION NUMBER: US/10/698,489

CURRENT FILING DATE: 2003-11-03

PRIOR FILING DATE: 2003-11-03

PRIOR FILING DATE: 2001-11-03

PRIOR FILING DATE: 2001-02-07

NUMBER OF SEQ ID NOS: 126

SOCTIMARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
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US-09-530-139-14
Sequence 14, Application US/09530139
Publication No. US20030092892A1
GENERAL INFORMATION:
APPLICANT: FRENKEN, LEON GERARDUS
APPLICANT: LEDEBOER, ADITANUS MARINUS
APPLICANT: LEDEBOER, ACGT, CORNELIS PAUL
TITLE OF INVENTION: MULTIVALENT ANTIGEN-BINDING PROTEINS
FILE REFERENCE: 60113/268075/ASH
CURRENT APPLICATION NUMBER: US/09/530,139
CURRENT FILING DATE: 2000-04-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1997-10-27
SOFTWARE: PATENTING DATE: 1997-10-27
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 53.1%; Score 17; DB 10; Length 6; Best Local Similarity 60.0%; Pred. No. 1e+06; Matches 3; Conservative 2; Mismatches 0; Indels
                  Query Match 53.1%; Score 17; DB 9; Length 6; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity
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2 VTVSS 6
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Patent No. US20020115136A1
GENERAL INFORMATION:
APPLICANT: MERKULOV et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001103
CURRENT APPLICATION NUMBER: US/09/777,921A
CURRENT FILING DATE: 2002-02-07
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 4.0
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                   Muyldermans, Serge
TITLE OF INVENTION: VARIABLE FRAGMENTS OF IMMUNOGLOBULINS -
USE FOR THERAPEUTIC OR VETERINARY PURPOSES
                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SPENCER & FRANK
STREET: 1100 New York Avenue, N.W., Suite 300 Bast
CITY: Washington
                                                                                                                                                                                                                   COUNTER: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/154,971

FILING DATE: 28-May-2002
CLASSIFICATION AUMBER: US/08/945,244

FILING DATE: 40nknown>
APPLICATION NUMBER: BP5400932.0

FILING DATE: 25-APR-1996
APPLICATION NUMBER: EP 95400932.0

FILING DATE: 25-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOILIN, Michael A.
REGISTRATION NUMBER: 31,957

REFERENCE/DOCKET NUMBER: GUPLA 0003
TELECOMMUNICATION INFORMATION:
TELEPONE: 202-414-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.1%; Score 17; DB 14; Length 5; 60.0%; Pred. No. 1e+06; 1ive 2; Mismatches 0; Indels
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TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-154-971-29
APPLICANT: Hamers, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 29
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                       COUNTRY: USA
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GRGANISM: Homo sapiens
US-09-777-921A-17
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1 VTVSS 5
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Sequence 108, Application US/09788006

Publication No. US20030036093A1

GENERAL No. US20030036093A1

GENERAL NO. US20030036093A1

APPLICANT: Klepeis, John L.

TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and

TITLE OF INVENTION: Polypeptide Tertiary Structures

FILE REPERENCE: PU-0007

CURRENT APPLICATION NUMBER: US/09/788,006

CURRENT APPLICATION NUMBER: US/09/788,006

CURRENT APPLICATION NUMBER: 2001-02-16

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PatentIn version 3.0

SEQ ID NO 108

LENGTH: 5
                                                                                                                                                                                                                                      Publication No. US20030036093A1
GENERAL INFORMATION:
APPLICANT: Floudas, Christopher A.
APPLICANT: Floudas, Christopher A.
APPLICANT: Klepeis, John L.
TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and TITLE OF INVENTION: Polypeptide Tertiary Structures
FILE REFERENCE: PU-0007.
FURRENT APPLICATION NUMBER: US/09/788,006
CURRENT PILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 107
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               56.2%; Score 18; DB 15; Length 7; 57.1%; Pred. No. 1e+06; 2; Indels tive
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                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Streptomyces griseus
US-09-788-006-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Streptomyces griseus
US-09-788-006-108
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75.0%;
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          Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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FTIDSSS 7
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1 FTVT 4
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US-10-154-971-29
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US-10-006-869-637

Sequence 637, Application US/10006869

Publication No. US20030082166A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

CURRENT APPLICATION NUMBER: US/10/006,869

CURRENT FILING DATE: 2001-12-03

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 637

LENGTH: 7
JULIAND TO SEQUENCE 11, Application US/10267565

Publication No. US20030204059A1

GENERAL INFORMATION:
APPLICANT: Gately, Maurice
APPLICANT: Humes, Jeffery
APPLICANT: Humes, Jeffery
APPLICANT: Humes, Jeffery
APPLICANT: Breakly Frank
TITLE OF INVENTION: DYRHCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: LYMPHOCYTE MATURATION FACTOR AND MONOCLONAL
TITLE OF INVENTION: LYMPHOCYTE NO/10267,565
CURRENT FILING DATE: 1999-00-1-23
PRIOR PELING DATE: 1999-00-2
PRIOR APPLICATION NUMBER: 08/459,151
PRIOR APPLICATION NUMBER: 07/857,023
PRIOR APPLICATION NUMBER: 07/857,023
PRIOR PELING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 07/857,033
PRIOR PELING DATE: 1999-06-09
PRIOR PELING DATE:
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative linear modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-10-006-869-637

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%; Score 18; DB 12; Length 7; 100.0%; Pred. No. 1e+06;
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Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 TLTI 5
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APPLICANT: Jiang, Ning
APPLICANT: Glang, Ning
APPLICANT: Kebir, Hania
APPLICANT: Kebir, Hania
APPLICANT: Lakowski, Bernard
APPLICANT: Lakowski, Bernard
ITLE OF INVENTION: CLK-2 NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
ITLE REFERENCE: 11202-006-999
CURRENT APPLICATION NUMBER: US/10/349,507
CURRENT PILLING DATE: 2003-01-22
PRIOR PILLING DATE: 2002-12-20
PRIOR PILLING DATE: 2001-06-20
PRIOR PILLING DATE: 2001-06-20
PRIOR PILLING DATE: 2000-06-22
PRIOR PILLING DATE: 2000-06-22
PRIOR FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-395-032-637

US-10-395-032-637

Sequence 637, Application US/10395032

Publication No. US20030229199A1

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C9

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 637

LENGTH: 7

LENGTH: 7

LENGTH: 7
                                                                              Gaps
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative linear modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
OTHER INFORMATION: recognition sequence
US-10-395-032-637
                                                                            ö
                   Score 18; DB 14; Length 7;
Pred. No. 1e+06;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 56.2%; Score 18; DB 14; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10349507
Publication No. US20030199002A1
GENERAL INFORMATION:
APPLICANT: Hekimi, Siegfried
Query Match
Best Local Similarity 57.1.
Thes 4; Conservative
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; ORGANISM: Homo sapiens
US-10-349-507-11
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June 1, 2004, 11:18:42 ; Search time 34.6667 Seconds (without alignments) 56.387 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/USO7_NEW
/cgn2_6/ptodata/1/pubpaa/USO6_NE
/cgn2_6/ptodata/1/pubpaa/USO6_PU
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/cgn2_6/ptodata/1/pubpaa/USO7_NEI
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/cgn2_6/ptodata/1/pubpaa/USO8_PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1151071 seqs, 279249464 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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32
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 18, Appl Sequence 11, Appl Sequence 637, App Sequence 11, Appl Sequence 107, App Sequence 107, App Sequence 108, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl
SUMMARIES	US-10-150-654A-18 US-10-150-654A-18 US-10-006-869-637 US-10-349-507-11 US-10-395-032-637 US-09-788-006-107 US-09-788-006-108 US-09-788-006-108 US-09-730-139-14 US-09-530-139-14 US-10-156-820-59 US-10-156-820-59 US-10-156-820-59 US-10-156-820-59 US-10-156-820-59 US-10-156-820-59
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Score	222 222 222 222 222 222 222 223 224 224
Result No.	44444444444444444444444444444444444444

o '	equence 69,	quence 164,	equence 164		quence 214	e 164	e 3,	e 4,	e 394	39,	equence 394	6, 1	equence 39,	Sequence 650, App	9	ý	405	e 402	402	e 65(24.2	•	e 47,	5,	124,	equence 7,	12,	equence 8,	equence 7, Appl
16 US-10-054-712-	9 US-09-83Z-7Z3-69	9 US-09-996-Z88-T64	10 US-09-996-265-1	14 US-10-303-331-6	14 US-10-022-06	15 US-10-461-863-1	14 US-10-286-18	14 US-10-286-18	14 US-10-315-9	14 US-10-317-251	14 US-10-317-252A-3	9 US-09-876-38	14 US-10-105-930-3	14 US-10-006-86	14 US-10-287-8	14 US-10-288-340-	14 US-10-315-964	14 US-10-317-251	14 US-10-	15 US-10-395-032-65	15 US-10-394-980-2	16 US-10-418-9	16 US-10-374-466-4	9 US-09-056-16	9 US-09-056-16	9 US-09-876-3	9 US-09-734-417-	-09-095-881-	9 US-09-947-137-
16 16 50.0	16 50.	16 50.	9 16 50.	0 16 50.	1 16 50.	2 16 50.	3 15 46.	4 15 46.	5 15 46.	6 15 46.	7 15 4	8 15 46.	9 15 46.	0 15 46.	15 46.	2 15 46.	3 15 46.	15 46.	46.	6 15 46.	15 46.	8 15 46.	15 46.	15 46.	15 46.	15 46.	15 46.	15 4	46.

ALIGNMENTS

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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: HANSEN, HANS J.
APPLICANT: HENNE, WILLIAM J.
APPLICANT: DEUNG, SHUI-ON
APPLICANT: QU, ZHENGXING
TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
TITLE OF INVENTION: USE WITH BI-SPECIFIC ANTIBODIES
TITLE REFERENCE: 018733-1085
CURRENT FILING DATE: 2002-12-17
FRIOR APPLICATION NUMBER: 09/382,186
FRIOR FILING DATE: 1999-08-23
FRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 18
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-150-654A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.8%; Score 22; DB 14; Length 6; Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 4; Conservative 2; Mismatches 0; Indels
                        Sequence 18, Application US/10150654A
Publication No. US20030198595A1
JS-10-150-654A-18
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|:|:| 1 TVTVSS 6

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amino acid residues of the first segment, together with an additional
amino acid residue(s), adjacent to the first amino acid sequence. The
beta-sheets and disulphide bridges of a polypeptide are determined by
identifying a superstructure encompassing alternative beta-strand
arrangements, representing the superstructure by an integer-linear
contact energy, and then solving the model. The method can
also apply energy modelling with a full atom force field potential to
generate a constrained global optimisation problem, optionally applying a
corptimisation problem to determine the three-dimensional structure of the
polypeptide and is useful for determining the tertiary structure
of a polypeptide and is accurate and reliable. The sequences presented in
ABU12184-ABU122235 are the pentapeptides of the Streptomyces griseus
immunoglobulin-binding domain from streptococcal protein G, 1GB1, which
were used to predict the alpha-helical regions in an example of the
constrains and securate and reliable. The area example of the
method of the invention
         8555555555555555555
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Sequence 5 AA;

ö Gaps ; 0 0; Indels Query Match 53.1%; Score 17; DB 6; Length 5; Best Local Similarity 75.0%; Pred. No. 1.4e+06; Matches 3; Conservative 1; Mismatches 0; Indels

1 FILT 4 ||:| 2 FTVT 5 ઠ 셤 Search completed: June 1, 2004, 11:16:14 Job time: 49.6667 secs

us-09-712-819c-1:closed.rag

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inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, chancing delivery of a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting concerning apoptosis in a nonclassical cadhering carporatesis in a mammal, inhibiting cell, preventing or treating obesity in a mammal, stimulating central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducts can also be used for treating e.g. psoriasis, arthritis, age products can also be used for detection and diagnosis and in bioreactors. AAY60592 to AAY64572 represent specifically claimed peptides, and the areas and an another the areas of the areas 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention
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Sequence 7 AA;

Gaps 0 Score 18; DB 3; Length 7; Pred. No. 1.4e+06; 1; Mismatches 2; Indels 56.2%; 4; Conservative Local Similarity Query Match Best Loc Matches

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1 FTLTISS 7 1 Fridss 7 ઠ g

ABB84102 standard; protein; 7 AA.

(first entry) 09-SEP-2002 ABB84102;

Human single chain diabody CEAGal fragment #2.

Antibody; multimer; cytostatic; detection; immunoassay; tumour.

Homo sapiens

Location/Qualifiers Key Misc-difference

/note= "Unidentified residue"

DE10060140-A1

06-JUN-2002.

04-DEC-2000; 2000DE-01060140

04-DEC-2000; 2000DE-01060140

(VECT-) VECTRON THERAPEUTICS IMT AG

Kontermann R;

WPI; 2002-520984/56.

New multimer of single-chain antibodies, useful e.g. for diagnosis drug delivery, has four variable chains linked through peptides of controlled length.

Example 1; Fig 2B; 16pp; German.

This invention describes a novel multimer containing at least two antibodies, each, independently, comprising a polypeptide chain of structure V1-PA-V2-PM-V3-PB-V4 where V1-V4 = variable domains; PA, PB and PM = peptide linkers with PA and PB containing 0 or 1 amino acid. The

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products of the invention have cytostatic activity. The multimers described can be used for diagnostic detection, in essentially standard immunoassay methods, and for binding at least one component and/or fused protein or peptide to a cell, especially to deliver a toxin or for infection, transformation or transfection of the cell. (I), or nucleic treating tumours. The multimers are relatively small (about 110 kDa for dimer) but have multiple binding sites to ensure high binding affinity. This sequence represents a fragment of the single chain diabody CEAGal (composed of a tumour marker carcinoembryonic antigen fragment and E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcal protein G, 1GB1, alpha helix prediction pentapeptide #51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTRO-FOLD; ab anitio; alpha-helix; beta-sheet; disulphide bridge; atomistic modelling; low energy conformation; entropic energy; free energy; equilibrium probability; helical cluster; integer-linear; mathematical model; hydrophobic contact energy; atom force field potential; global optimisation; torsion angle; dynamic algorithm; three-dimensional structure; tertiary structure; immunoglobulin-binding domain; protein G; 1GB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining helix regions, and beta sheets of polypeptide, involves partitioning peptide, atomistic modeling by selected force, generating ensemble low energy, and calculating free energies for each peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 5; Length 7; Pred. No. 1.4e+06; 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU12234 standard; peptide; 5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                         invention
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ID ABU1234
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AC ABU122
XX
DE Strep
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WPI; 2000-038791/03.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                             Sequence 7 AA;
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20-JAN-1999;
08-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulation;
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                                                                                                                       ABR55412-20 represent conserved region of a phospholipase C (PLC)-zeta polypeptide. PLC-zeta polypeptides are capable of triggering calcium oscillations in oocytes. The PLC-zeta isoform is expressed specifically in mammalian sperm, and is an essential protein for mammalian fertilisation and embryo development. PLC-zeta polynucleotides are useful for preparing a composition for diagnosing or treating infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated antibody has been developed which binds specifically to cytotoxic lymphocyte maturation factor (CLMF) and neutralises CLMF induced proliferation by more than 50% in a CLMF dependent T cell growth assay and/or inhibits binding of at least 60% of the factor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic lymphocyte maturation factor; CLMF; cytokine; synergize; interleukin 2; IL-2; human; lymphoblastoid cell; detection; purifying; proliferation; cytotoxic T cell; transplantation; antibody.
                                                          New phospholipase C-zeta gene, useful for preparing a composition for diagnosing or treating infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies to cytotoxic lymphocyte maturation factor - useful for detecting, purifying, and/or blocking proliferation and activation of cytotoxic T cells, such as in transplantation(s).
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                     56.2%; Score 18; DB 6; Length 5; 100.0%; Pred. No. 1.4e+06; 1.4e+06; live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tryptic 40 kD subunit CLMF peptide off PVDF #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gately MK,
                                                                                                Claim 10; Page 68; 107pp; English
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                                                                                                                                                                                                                                                                                                                                                                              AAW58711 standard; peptide; 7 AA.
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90US-00520935.
90US-00572284.
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94US-00205011.
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Gubler UA,
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
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                                    WPI; 2003-421400/39
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                                                                                                                                                                                                               Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5780597-A.
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                                                                                                                                                                                                                                                                                                                                                                                                         AAW58711;
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         Lai T,
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AAW58711
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phytohaemagglutinin (PHA) activated peripheral blood lymphocyte (PBL) blasts as determined in a CLMF receptor binding assay. CLMF is a heterodimeric protein having a molecular weight band of 75 kD, determined by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) under non-reducing and/or reducing conditions, providing a first subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight band of 40 kD and a second subunit having a molecular weight of 35 kD. The present sequence represents a tryptic 40 kD CLMF peptide off polyvinylidene diflucinde (PVDF), from an example of the present invention. The antibody can be used for the purification and/or detection of CLMF. It is also used in therapeutic treatments which require selective blocking of proliferation and activation of cytotoxic T cells (CTLs) such as in transplantation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin, cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoclein; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nonclassical cadherin mediated cell adhesion; CAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Le
1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.2%; Score 18; DB 100.0%; Pred, No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY64225 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to diagnosing the presence of colon cancer, metastases of colon cancer, staging colon cancer, monitoring colon cancer for the onset of metastasis or monitoring a change in stage of colon cancer in a patient. The method involves determining a colon specific gene (CSG) in cells, tissues or bodily fluids and comparing it with levels of CSG in cells, tissues or bodily fluids from a normal human control. Colon cancer can be treated by administering a molecule which down regulates the expression or activity of CSG. An immune response against a target cell expressing CSG can be induced by delivering an immune response is mounted. Therapeutic agents are useful for imaging an immune response is mounted. Therapeutic agents are useful for imaging colon cancer in a patient by administering an agent labelled with paramagnetic ions or a radioisotope to the patient. They are also useful for preventing the onset of colon cancer, and in diagnosis and treatment of the disease. Sequences AAU85424-AAU85502 represent human colon specific protein antibody binding sites used in the method of the
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon specific polypeptide antibody binding site #31.
  Score 21; DB 3; Length 7;
Pred. No. 1.4e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon specific gene; CSG; cytostatic; metastasis; colon cancer staging; antibody binding site.
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                                                                                                                                                                                                                                                                                                     AAU85454 standard; peptide; 5 AA.
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Query Match 65.6%;
Best Local Similarity 66.7%;
Matches 4; Conservative
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YSLTIS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                            AAU85454;
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An injury healing and postsurgical tissue recovering integrin activating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.4%; Score 19; DB 4; Length 6; 60.0%; Pred. No. 1.4e+06; ive 2; Mismatches 0; Indels
                                                                                                                              Integrin stimulant; vulnerary; injury healing; postsurgical tissue recovery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYWA-) UNIV WALES COLLEGE OF MEDICINE.
                                                                                             Integrin activating peptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR55418 standard; peptide; 5 AA.
AAM51422 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             (HISM ) HISAMITSU PHARM CO LID
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28-JUN-2002; 2002GB-00014945.
                                                                                                                                                                                                                                                                                                              31-JAN-2000; 2000JP-00022469.
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                                                              (first entry)
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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                             JP2001213898-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6 AA;
                                                                                                                                                                              Unidentified.
                                                              08-JAN-2002
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                               AAM51422;
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ABR55418
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Gaps

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Query Match 62.5%; Score 20; DB 5; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 4; Conservative 0; Mismatches 0; Indels

1 FTLT 4 |||| 2 FTLT 5

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hoogenboom H,
                                                                                                                 Disclosure; Page 15; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 6; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                 AAY40735 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour; chemotherapeutic agent
                                                                                                                                                                                                                                             Query Match 75.0%;
Best Local Similarity 83.3%;
Matches 5; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98EP-00870065
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
          (INNO-) INNOGENETICS NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INNO-) INNOGENETICS NV
                              Hufton S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desmet J, Hufton S,
                                                   WPI; 2000-665002/64
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                                                                                                                                                                                                                                                                                                    FTLSIS
                                                                                                                                                                                                                         Sequence 7 AA;
                                                                                                                                                                                                      the invention
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                              Desmet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                     AAY40735;
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Query Match Best Local Similarity 66.7 Matches 4; Conservative (INNO-) INNOGENETICS NV. Hufton S, WPI; 2000-665002/64. ø 1 FTLTIS WO200060070-A1. Sequence 7 AA; 01-APR-1999; 01-APR-1999; 12-OCT-2000 Desmet J, Synthetic. AAB30073; RESULT 8 8888888888888888888888888888888888 ઠે g ö The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments. New scaffold protein, useful for stabilizing antigens used as vaccines. Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; Gaps ó 84 derivative #9, beta strand of scaffold protein structure. Score 24; DB 3; Length 7; Pred. No. 1.4e+06; Mismatches 0; Indels Sablon E; Sablon Hoogenboom H,

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form two beta sheets $1/$4/$3 and $6/$5/$2 with each strand connected to
the next by hydrogen bonds, which generate a beta sandwich architecture.

If the additional beta strands Al-A3 are included in the structure the
scaffold is constructed of two beta sheets, with the structures the
conformation and $6/$5/$2/$2/$3. The beta strands are connected to each
other via amino acid loops, where at least one of the loops binds to a
receptor or antigen. The scaffold protein is used to stabilize antigens
or whole proteins such as receptors, or their fragments. It may be used
to bind two separate molecules. For example, one surface of the scaffold
may be bound to a protein which binds to a tumour antigen. This will
carpet the complex to tumour cells. Another surface may be bound to a
cytotoxic molecule or an autoimmune antibody which may then kill the
tumour cells. Therefore the scaffold protein may be used to target
chemotherapeutic agents to specific cells. It may also be used to
stabilize individual peptides in a peptide library and may be used in
diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 21; DB 2; Length 7;
Pred. No. 1.4e+06;
?; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scaffold protein SCA S4 peptide SEQ ID NO: 134.
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Sequence 7 AA;

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98EP-00870065

98EP-00870065

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Desmet J, Hufton S,
                                        INNO-) INNOGENETICS
                                                                          WPI; 1999-542958/46.
                      31-MAR-1998;
    31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                           The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as a scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of
                                                                                                                                                                                                                                                                     Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                 Human, CTLA-4; scaffold protein; antigen-binding; receptor-binding;
SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis;
diabetic retinopathy; atherosclerosis.
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                                                                 Scaffold protein SCA S4 peptide SEQ ID NO: 136
                                                                                                                                                                                                                                   Hoogenboom H, Sablon E;
                                                                                                                                                                                                                                                                                                           Disclosure; Page 15; 68pp; English
            AAB30075 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY40736 standard; peptide; 7 AA.
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                                                                                                                                                                                               99WO-EP002283
                                              (first entry)
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                                                                                                                                                                                                                (INNO-) INNOGENETICS NV.
                                                                                                                                                                                                                                   Desmet J, Hufton S,
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                                                                                                                                       WO200060070-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                    the invention
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                                               09-FEB-2001
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                                                                                                                       Synthetic.
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                              AAB30075;
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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40605) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with he structures of scaffold is constructed of two beta sheets, with the structure of scaffold is constructed of two beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold protein is used to stabilize antigens or whole proteins which hinds to a tumour antigen. This will the complex to tumour cells. For example, one surface may be bound to a protein which hinds to a tumour antigen. This will the tumour cells. Therefore the scaffold protein may then kill the contour cells. Therefore the scaffold protein may be used to target the complex to specific cells. It may also be used in the stabilize individual peptides in a peptide library and may be used in the stabilize antigens used as vaccines
New scaffold protein, useful for stabilizing antigens used as vaccines
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                                                                               Disclosure; Page 6; 105pp; English.
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FTLSIS 7
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or whole proteins such as receptors, or their fragments. It may be used to bind two separate molecules. For example, one surface of the scaffold may be bound to a protein which binds to a tumour antigen. This will target the complex to tumour cells. Another surface may be bound to a cytotoxic molecule or an autoimmune antibody which may then kill the tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to specific cells. It may also be used to stabilize individual peptides in a peptide library and may be used in diagnostic techniques, and to stabilize antigens used as vaccines
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding; SCA domain; cancer; thrombosis; osteoporosis, rheumatoid arthritis; diabetic retinopathy; atherosclerosis.
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                                                                                                                                                              Query Match 87.5%; Score 28; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Scaffold protein SCA S4 peptide SEQ ID NO: 137.
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                                                                                                                                                                                                                                                                                                                AAB30076 standard; peptide; 7 AA.
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FTLTIS 7
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                                                                                                                                      Sequence 7 AA;
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AAB30076
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New scaffold protein, useful for stabilizing antigens used as vaccines.

Disclosure, Page 6, 105pp, English.

Desmet J, Hufton S, Hoogenboom H, Sablon E;

WPI; 1999-542958/46.

98EP-00870065.

31-MAR-1998; 31-MAR-1998;

EP947582-A1. 06-OCT-1999

Synthetic.

INNO-) INNOGENETICS NV.

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.

S4 derivative #11, beta strand of scaffold protein structure.

(first entry)

01-DEC-1999

AAY40737;

AAY40737 standard; peptide; 7 AA.

RESULT AAY40737

FTLTIS

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Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-Y40609) together form a single-chain scaffold protein which contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands of the next by hydrogen bonds, which generate a beta sandwich architecture. Cc functionally equivalent derivative of these sequences. The beta strands of the next by hydrogen bonds, which generate a beta sandwich architecture. Cc the next by hydrogen bonds, which generate a beta sandwich architecture. Cc the next by hydrogen bonds, which generate a beta sandwich architecture. Cc the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structure the caffold is constructed of two beta sheets, with ene structures. A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to other via amino acid loops, where at least one of the loops binds to a receptor or antigens. The scaffold protein is used to stabilize antigens to bind two separate molecules. For example, one surface of the scaffold connected to complex to tumour cells. Therefore the scaffold protein may be used to target tumour cells. Therefore the scaffold protein may be used to target chemotherapeutic agents to a peptide library and may be used in cynther surface individual peptides in a peptide library and may be used in cynthers antigens used as vaccines
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Matches 5; Conservative
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87.5%; Score 28; DB 3; Length 7; 100.0%; Pred. No. 1.4e+06; live 0; Mismatches 0; Indels

Query Match Best Local Similarity lov. ---- 6; Conservative

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Sequence 7 AA;

The present invention is concerned with producing scaffold proteins based upon the human CTLA-4 SCA domain. These scaffold proteins can be used as scaffold to bind antigen- or receptor-binding fragments. These can be used in the treatment of diseases such as cancer, atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and diabetic retinopathy. Sequences AAB29930-B29939 were used in the production of the proteins of the invention

Scaffold composed of single-chain polypeptide having beta sandwich architecture carrying new and randomized peptide sequences useful as supporting framework and carrying antigen- or receptor binding fragments.

Disclosure; Page 15; 68pp; English.

RESULT 4

Copyright (c) 1993 - 2004 Compugen Ltd.	Run on: June 1, 2004, 10:40:31 ; Search time 45.6667 Seconds (without alignments) 43.310 Million cell updates/sec	Title: US-09-712-819C-1 Perfect score: 32 Sequence: 1 FILIISS 7	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1586107 seqs, 282547505 residues	Total number of hits satisfying chosen parameters: 92273	Minimum DB seq length: 0 Maximum DB seq length: 7	
			score:		core: able:	core: able: ber of	Run on: June 1, 2004, 10:40:31; Search time 45.6667 Seconds (without alignments) 43.310 Million cell updates/sec Title: US-09-712-819C-1 Sequence: 1 FTLTISS 7 Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5 Searched: 1586107 seqs, 282547505 residues Total number of hits satisfying chosen parameters: 92273 Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay40738 S4 deriva	6 Sca	~	5 Scaf		4 Sca	\$34	ഷ	_	2 Integr	α	11 Trypti	Ŋ	ď	4 Strept	35	53 H	Aaw75358 Hexapepti		32		Aay40723 S3 deriva	062 Sca	1200 H11	205 H11
	AAY40738	AAB30076	AAY40737	AAB30075	AAY40736	AAB30074	AAY40735	AAB30073	AAU85454	AAM51422	ABR55418	AAW58711	AAY64225	ABB84102	ABU12234	ABU12235	AAW39453	AAW75358	AAW75290	AAE31832	AAR07656	AAY40723	AAB30062	AAM44200	AAM44205
DB	7	m	N	m	N	ო	N	m	ហ	4	φ	~	m	Ŋ	φ	9	N	~	N	ø	7	~	m	4,	4
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Score	28	128	25	25	24	24	21	21	20	19	18	18	18	8 T ·	17	17	17	17	17	17	17	17	17	17	17
Result No.		α	m	44	ഗ	w	7	60	9	0 ۲	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25

Aap93345 Portion o	Aar93089 GAL4 DNA	Aaw61443 Gal 4 pro	Aaw76753 Murine si	Aaw92487 Murine Ga	Aay90491 GAL4 DNA	Aab03571 Nuclear c	Aab36961 Peptide #	Aab60836 Peptide #	Abj11455 Human 125	_	Abu72693 Novel pro	Abr45358 Staphyloc	Abr46478 Staphyloc	Abr44966 Staphyloc	Abr45694 Staphyloc	Abr46870 Staphyloc		Abj57003 184P1E2-r	Aar72775 Mammalian
AAP93345	AAR93089	AAW61443	AAW76753	AAW92487	AAY90491	AAB03571	AAB36961	AAB60836	ABJ11455	AAE28111	ABU72693	ABR45358	ABR46478	ABR44966	ABR45694	ABR46870	ABR46086	ABJ57003	AAR72775
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16	16	16	16	16	16	16	16	16	. 16	16	16	16	16	16	16	16	16	16	16
56	27	28	50	30	31	32	33	34	35		37	38	39	40	41	42	43	44	45

ALIGNMENTS

S4 derivative #12, beta strand of scaffold protein structure. AAY40738 standard; peptide; 7 AA. 01-DEC-1999 (first entry) AAY40738;

Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine; tumour; chemotherapeutic agent.

EP947582-A1. Synthetic.

98EP-00870065. 98EP-00870065 31-MAR-1998; 31-MAR-1998; 06-OCT-1999.

Hoogenboom H, Sablon E; Desmet J, Hufton S, WPI; 1999-542958/46.

(INNO-) INNOGENETICS NV.

New scaffold protein, useful for stabilizing antigens used as vaccines. Disclosure; Page 6; 105pp; English. Sequences AAY40727-Y40748 are functionally equivalent derivatives of the S4 peptide (AAY40607) which forms part of a scaffold protein. S4 is a beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-12 beta strand peptide which forms part of a beta sheet. Peptides (AAY40601-12 beta strand peptide bond, contains less than 10% alpha helix and contains at least 1 disulfide bond, contains less than 10% alpha helix and contains at least 6 beta-strands. The scaffold protein is constructed of beta strands S1-S6, and may also include beta strands A1-A3, or any functionally equivalent derivative of these sequences. The beta strands form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to the next by hydrogen bonds, which generate a beta sandwich architecture. If the additional beta strands A1-A3 are included in the structure the scaffold is constructed of two beta sheets, with the structures A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each other via amino acid loops, where at least one of the loops binds to a receptor or antigen. The scaffold is used to stabilize antigens

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MEDLINE=95313343; PubMed=7793062;
Vicek C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,
Letchworth G.J., Schwyzer M.;
"Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus 1 genome which exhibits a colinear gene arrangement with
the UL21 to UL4 genes of herpes simplex virus.";
Virology 210:100-108(1995).
EMBL; Z48053; CAA88130.1; -.
Hypothetical protein.
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P83492;
P83492;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).
Bionectria ochroleuca (Gliocladium roseum).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
NCBI_TaxID=29856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang K.;
Zhang K.;
Submitted (DEC-2002) to Swiss-Prot.
Submitted (DEC-2002) to Swiss-Prot.
-!- FUNCTION: ACTS AS A SERINE PROTEASE.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.
GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
InterPro; IPR000209; Peptidase endopeptidase activity; NAS.
RROSITE; PS00136; SUBTILASE ASP; PARTIAL.
RROSITE; PS00137; SUBTILASE SER; PARTIAL.
RHOGOIDS; Serine protease.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Bovine herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
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Q65578;
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21.9%; Score 7; DB 12; Length 7;

Query Match

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Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps
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4 TISS 7

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8 8

Search completed: June 1, 2004, 11:18:36 Job time: 33.3333 secs

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6321B415B05DB000 CRC64;
    6 AA; 675 MW;
                               Query Match
Best Local Similarity 100...
Sinconservative
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01-FEB-1997 (
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ID Q4702
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DT 01-NO
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DE AAD A
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XERAIN=CV. ALWARO; TISSUE=Leaf;

XERAIN=CV. ALWARO; TISSUE=Leaf;

XERAIN=CV. ALWARO; TISSUE=Leaf;

XERAIN=CV. ALWARO; PubMed=10874046;

Xemaguchi K., Subramanian A.R.;

Yemaguchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 275:28466-28482 (2000).

J. Biol. Chem. 275:28466-28482 (2000).";

J. Biol. Chem. 275:28406-28482 (2000).

GO: GO:0003735; F:RNA binding; IEA.

GO: GO:0003735; F:RNA binding; IEA.

RO: GO:0003735; R:Structural constituent of ribosome; IEA.

InterPro: IPR002363; Ribosomal L10eub.

RROSITE; PS01109; RIBOSOMAL L10; PARTIAL.

RADOSOMAL L10; PARTIAL.

RADOSOMAL L10; PARTIAL.
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2000 (TrEMBLrel. 15, Last annotation update)
Chloroplast 50S riboscomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinacia Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.
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Matches
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P82182
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"Characterization of the cmcH genes of Nocardia lactamdurans and Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem O-carbamoyltransferase for cephamycin biosynthesis."; Gene 162:21-27(1995).
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MEDLINE=94079349; PubMed=8257126;
MEDLINE=94079349; PubMed=8257126;
Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
"Analysis of the aac(3)-VIa gene encoding a novel 3-N-
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MEDLINE=96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.
Liras P.;
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Enterobacteriaceae, Enterobacter.
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Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
NCBI_TaxID=1913;
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    Length
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Aad Al protein (Fragment).
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Last annotation update)
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EMBL; M88012; AAA16193.1; -.
NON_TER 1
25.0%; Score 8; DB 10;
100.0%; Pred. No. 1e+06;
tive 0; Mismatches 0
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01-FEB-1997 (TrEMBLrel. 02, Last seque
01-DEC-2001 (TrEMBLrel. 19, Last annot
3'-methylcephem hydroxylase (Fragment)
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RESULT 6
P8353
ID P835
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P82445;
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10. JUN-2014 wall protein (Fragment).
Nicotiana tabacum (Common tobacco).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Nicotiana.
NICOTIANIE TAXID=4097;
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MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
Hoffmann D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; AAK32344.1; -.
NON TER 1 1 885 MW; 76C37731A046C700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
STRAIN=cv. PETIT HAVANA;
Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
"Protecmic study of secondary cell wall proteins from transformed
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QBJEB1;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676;
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-!- SUBCELLULAR LOCATION: CELL WALL.
-!- TISSUE SPECIFICITY: XYLEM.
GO; GO:0005618; C:cell wall; IEA.
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Best Local Similarity 33.3
Matches 1; Conservative
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Planta 0:0-0(200
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P82181;
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AC P8218:
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Q8JE81
            SO CE THE SECTION OF 
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MEDLINE=99231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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STRAIN-DSM 20451;
PubMed=12112860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
Thigh pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANBOUS: ON THE 2D-GBL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
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007354;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nifk (Fragment).
Nifk (Fragment).
Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
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P83533,
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI TaxID=1625;
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SEQUENCE 6 AA; 590 MW; 6DDD452D1AAC000 CRC64;
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Microbiology 145:743-753(1999).
EMBL; AF003700; AAC35193.1; -.
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STRAIN=N2-3-11;
MEDLINE=20011291; PubMed=10542330;
Medline 20011291; PubMed=10542330;
Poehling S., Piepersberg W., Wehmeier U.F.;
Manalysis and regulation of the secY gene from Streptomyces griseus N2-3-11 and interaction of the SecY protein with the SecA protein.";
Blochim. Biophys. Acta 1447:298-302(1999).
EMBL; X95915; CAA65160.1; -.
EMBL, X95915; CAA65160.1; -.
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PubMed=12112860;
Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
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P83530;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI TaxID=1625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces griseus.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=1911;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Best Local Similarity
Matches 2; Conserv
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                                 1 FTL 3
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5 FTV 7
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Q54248;
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Kim Y.-C.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88298; AAB66311.1; -.
GO; GO:0016702; F:oxidoreductase activity, acting on single d. . .; IEA.
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
1918_TaxID=6239;
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                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
NCBI_TaxID=56193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.5%; Score 12; DB 2; Length 7; 20.0%; Pred. No. 1e+06; artive 4; Mismatches 0; Indels
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STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043704; AAO38592.1; -.
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DBS041A6F0 CRC64;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein WO1B11.6.
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SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;
                                                                                                       Catechol-2, 3-dioxygenase (Fragment)
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                       Sphingomonas chungbukensis.
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Best Local Similarity 20.0
Matches 1; Conservative
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P82541 spinacia ol 050556 actinobacil Q8kms9 enterobacte 015903 homo sapien 098866 spinacia ol 095845 saccharomyc 090535 arabidopsis Q8k3h6 rattus norv 097410 transmissib 042564 fugu rubrip P83073 bacillus ce Q8kms3 klebsiella Q47505 escherichia bu Q84112 borrelia bu Q84112 borrelia bu Q84112 horrelia bu Q84104 borrelia bu Q84104 borrelia bu Q84103 lycopersico Q5368 rattus sp. Q5368 sepia offic Q08433 rattus sp. P83569 sepia offic Q08433 rattus sp. Q83509 borrelia bu Q8mh7 homo sapien P92293 hordeum vul P92293 hordeum vul

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MEDLINE-5,
MEDLINE-5,
MEDLINE-96427318; PubMed=8830682;
Rehm B.H.A., Ertesvag H., Valla S.;
Rehm B.H.A., Ertesvag H., Valla S.;
Rehm B.H.A., Ertesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL; X87973; CAA61230.1; -.
NON TER

1 1
SEQÜENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Azotobacter vinelandii.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 50.0%; Score 16; DB 2; Length 7; Best Local Similarity 75.0%; Pred. No. 1e+06; Matches 3; Conservative 1; Mismatches 0; Indels
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Last sequence update)
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P82541
O50556
Q8KMS9
Q15903
O98866
Q95945
Q9C5B3
Q8K3H6
                                                                                                                          Q9YQ10
Q42564
P83073
Q8KMS3
Q47505
Q8GL12
Q8GL04
Q8MFY6
P93268
Q63668
Q67113
Q07624
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P83569
Q8GL00
Q8NHH7
Q15897
P92214
P92393
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01-FEB-1997 (TrEMBLrel. 02, Cr
01-FEB-1997 (TrEMBLrel. 02, Le
01-DEC-2001 (TrEMBLrel. 19, Le
AlgT protein (Fragment).
                                                                PRELIMINARY;
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034028;
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034028 sphingomona
Q7z1c0 caenorhabdi
054248 streptomyce
P83530 lactobacill
P83533 lactobacill
007354 synechococc
P82445 nicotiana t
08je81 human immun
P82181 spinacia ol
P72081 nocardia la
047029 enterobacte
P83492 bionectria
Q65578 bovine herp
                                                                                                      June 1, 2004, 10:53:46 ; Search time 31.3333 Seconds (without alignments)
70.488 Million cell updates/sec
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               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                            - protein search, using sw model
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034028
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sp.virus:*
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Gapop 10.0 , Gapext 0.5
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Match Length
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"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation.
MOD_RES 7 7 AMIDATION.
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Eur. J. Biochem. 250:727-734(1997).

-!- FUNCTION: May act as a neurotransmitter or neuromodulator.

-!- SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation; Multigene family.

MOD RES

7 AMIDATION.

SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Tortricoidea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Carcinustatin 5.
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Pubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.0%; Score 8; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; cive 0; Mismatches 1; Indels
                                                  1; Indels
Score 8; DB 1; Length 7; Pred. No. 1.4e+05;
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                            Pred. No. 1.4e+05;
0; Mismatches 1
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 7.
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MEDLINE=98054539; PubMed=9392829;
25.0%;
Query Match
Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 66.7
Les 2; Conservative
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P82158;
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels
Best Local Similarity 66.7%;
Matches 2; Conservative
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Search completed: June 1, 2004, 11:16:49 Job time : 9.66667 secs

Length 7;

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Similarity 2; Conserv
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P81807;
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Query Match
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P81806;
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ALL3_CARMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Myotropic peptide. May be important in the stimulation of ion transport and inhibition of diuretic activity in Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                                                                                                                                                                                                                                 Locusta migratoria (Migratory locust).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD RES
7 AMIDATION (POTENTIAL).
SEQUENCE 7 AA; 770 MW; 672879CDCB5DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Corpora cardiaca;
MEDLINE=92262851; PubMed=1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca, Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura, Eubrachyura, Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.0%; Score 8; DB 1; Length 6; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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Carcinus maenas (Common shore crab) (Green crab)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                               6 AA.
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PIR; A61068; A61068.
Neuropeptide; Amidation.
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SEQUENCE
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Eur. J. Biochem. 250:727-734(1997).

-!- FUNCTION: May act as a neurotransmitter or neuromodulator.

-!- SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Multigene family.

SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thorpe A.;
"Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator..!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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MEDLINE=98121193; Pubmed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Carcinus maenas (Common shore crab) (Green crab).

Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;

Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura;

Eubrachyura, Portunoidea, Portunidae, Carcinus.
                                                             1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.0%; Score 8; DB 1; Le 66.7%; Pred. No. 1.4e+05; rative 0; Mismatches 1;
Score 8; DB 1; Le
Pred. No. 1.4e+05;
); Mismatches 1.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                         7 AA.
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25.0%;
                                                             Conservative
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MEDLINE=89006280; Pubmed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
-! - CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
-! - CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
-! - SIMILARITY: Belongs to the biotin and lipoic acid synthetases family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21922; -; NOT_ANNOTATED_CDS.
PIR; 140698; 140698.
Biotin biosynthesis; Iron-sulfur; Transferase.
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nes 1; Conservative
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Daucus carota (Carrot)
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NCBI_TaxID=4039;
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MOD_RES
MOD_RES
SEQUENCE
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PSK_DAUCA
ID PSK_D
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 "Isolation and structure of the Streptococcus faecalis sex pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
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Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD RES
5 AMIDATION (POTENTIAL).
SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                         -!- MISCELLANGOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFICITY OF PHEROMONES TO PLASMIDS.
-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Cerebral ganglion, and Thoracic ganglion;
MEDLINE=98121193; PubMed=9461295;
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
               CAM373.";
FEBS Lett. 206:69-72(1986).
-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.
HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca,
Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura,
Eubrachyura, Portunoidea, Portunidae, Carcinus.
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01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Biotin synthase (EC 2.8.1.6) (Biotin synthetase) (Fragment)
                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                                                                                                                                                                                                      Length 7;
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                                                                                                                                                                                                                                   7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
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                                                                                                                                                                                                                                                                                  28.1%; Score 9; DB 1; Le 66.7%; Pred. No. 1.4e+05;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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AC P12937;
DT 01-JAN-1990
DT 01-JAN-1990
DT 28-FEB-2003
DE Biotin synth
GN BIOB.
OC Bacteria; Pro
OC Bacteria; Pro
OC Enterobacter
OX NCBI_TAXID=5
RN [1]
RP SEQUENCE FRO
                                                                                                                                                                                                         Pheromone.
SEQUENCE
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AL14 CARMA
ID AL14 CARMA
ID 30-MAY-
DT 30-MAY-
DT 30-MAY-
DT 30-MAY-
DE Carcin,
OC Eumalac
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
                                                                                                                                                                                                                                                                                                                                                                                           PSK_DAUCA STANDARD; PRT; 5 AA.

PS8261;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-

embryos.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: Sulfation is important for activity and for the binding to putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.

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MEDLINE=20212743; PubMed=10750705;
Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
Kamada H., Sakagami Y.;
"A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";
Plant Cell Physiol. 41:27-32(2000).
-!- FUNCTION: In presence of 2,4-D, stimulates proliferation of the
cells, but does not stimulate differentiation into the somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                        0; Indels
Match 25.0%; Score 8; DB 1; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+05; es 2; Conservative 0; Mismatches 0; Indele
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5 AA; 687 MW; 76C1BB504B300000 CRC64;
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SULFATION.
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cCF10.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIA_ENTFA STANDARD; PRT; 7 AA.

P11932;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=89008313; PubMed=3139658;
MCTIME=89008313; PubMed=3139658;
MOTIME, Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
Adsit J.C., Dunny G.M., Suzuki A.;
"Structure of cCF10, a peptide sex pheromone which induces
conjugative transfer of the Streptococcus faecalis tetracycline
resistance plasmid, pCF10.";
J. Biol. Chem. 263:14574-14578(1988).
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PCF10.
                                TISSUE=Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
MEDLINE=87005252; PubMed=3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada
White B.A., An F.Y., Clewell D.B., Suzuki A.;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 31.2%; Score 10; DB 1; Length 5; Best Local Similarity 33.3%; Pred. No. 1.4e+05; Matches 1; Conservative 2; Mismatches 0; Indels
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                                                                                                                                          rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
MOD RES 5 5 AMIDATION.
SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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CCF1_ENTFA
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CIA ENTRA
ID CIA E
AC 01193
DT 01-0C
DT 01-0C
DT 01-FE
DE Sex P
OS Enter
OX NCBI
COX NCBI
RN SEQUE
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RA MOXI
RA White
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"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
activity.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.";
Aust. J. Chem. 52:639-645(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Litoria rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
NCBI_TaxID=104895;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
NCBI_TaxID=104895,
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.4%; Score 11; DB 1; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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        MOD RES
        5
        AMIDATION.

        SEQUENCE
        5 AA; 656 MW; 71A9C9CB10300000 CRC64;

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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rubellidin 3.2.
Litoria rubella (Desert tree frog).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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RE32_LITRU
DR RE32_LITRU
AC P82073;
DT 28-FEB-2003
DC Amphibia; Bai
OC Amphibia; Bai
OC Amphibia; Bai
OC Amphibia; Bai
CC Amphibian de:
CC -!- FUNCTION
CC -!- TISSUE
C
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RESULT 4
E104 LITRU
ID E104 LITR
AC P82100;
DT 28-FEB-2(
DT 28-FEB-2(
DT 10-OCT-2(
DE BIECTIN
OS LITORIA
OC BURARYOU
OC PEIOGRY
OX NCBI TAX:
RN [1]

Matches

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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June 1, 2004, 10:41:50 ; Search time 7.66667 Seconds (without alignments) 47.542 Million cell updates/sec Run on:

US-09-712-819C-1 32 1 FTLTISS 7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	mus musculu	_	_	~	enterocc				daucus caro	Н	carcinus	O	O	carcinus	O							hirudo me						anthopleura	octopus min	litoria rub	· u	pardachirus	litoria rub
	Description	P99025	P82072	P82073	P82100	P20104	P11932	P81817	P12997	P58261	P41491	P81805	P81806	P81807	P81808	P82158	P80630	P02731	P36515	P13071	P81351	P35904	P42562	P42563	P58705	P42561	P58707	P01162	P58706	P58648	P82099	4185	P81864	82
SOFTES		RP_MOUSE	RE31_LITRU	32_LITRU	04_LITRU	71_ENTFA	CIA_ENTFA	AL14_CARMA	OB_CITFR	PSK_DAUCA	(1_LOCMI	ALL2_CARMA	3 CARMA	54_CARMA	JS_CARMA	ALL7_CYDPO	UC24_MAIZE	EOSI_HUMAN	RM01_YEAST	BIOA_CITFR)6_CLOPA	11_ACHFU	FAR3_HIRME	FAR4_HIRME	FFKA_ANTEL	FLRF_HIRME	FLRN_ANTEL	FMRF_MACNI	FYRI ANTEL	1)3_LITRU	I "I		.1_LITRU
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P82071 litoria rub P19991 acheta dome P54714 canis famil P80628 zea mays (m P13736 mytilus edu P13737 mytilus edu P82096 litoria rub P41966 moniezia ex P31889 ascaris suu P41871 helisoma tr P83274 macrobrachi P38499 procambarus	
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ALIGNMENTS

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28K ubiquitin-immunoreactive protein - inky cap (Coprinus cinereus) (fragment)
C;Species: Coprinus cinereus
C;Species: Coprinus cinereus
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 30-Sep-1993
C;Accession: A43766
R;Kanda, T.; Inoue, M.; Akiyama, M.;
Biochimie 72, 355-359, 1990
A;Title: Purification and characterization of an ubiquitin-immuno-reactive protein local
A;Reference number: A43766, MUID:91002724; PMID:1698461
A;Accession: A43766
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <KAN>
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5 ISS 7
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5 TL 6
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Search completed: June 1, 2004, 11:19:23 Job time: 12.6667 secs

3 05:58:33 2004

🧳 Thu Jun

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Systems of the strabrachion heavy chain - Staphylothermus marinus (fragment)
C;Species: Staphylothermus marinus
C;Species: Staphylothermus marinus
C;Species: Staphylothermus marinus
C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 17-Mar-1999
C;Accession: S69237
R;Peters, J; Nitsch, M; Kuehlmorgen, B; Golbik, R; Lupas, A; Kellermann, J; E
J, Mol. Biol. 245, 385-401, 1995
A;Fitle: Tetrabrachion: a filamentous archaebacterial surface protein assembly of ur
A;Reference number: S69237
A;Molecule type: protein
A;Residues: 1-5 <PET>
A;Residues: 1-5 <PET>
A;Residues: cell wall; glycoprotein; heat-stable protein
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S14159
parasporal crystal protein CryIC - Bacillus thuringiensis (fragment)
N;Alternate names: delta-endotoxin
C;Species: Bacillus thuringiensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: S14159
R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.
Eur. J. Biochem. 195, 631-635, 1991
A;Title: Two structural domains as a general fold of the toxic fragment of the Bacil A;Reference number: S14087; MUID:91153300; PMID:1847865
A;Accession: S14159
A;Molecule type: protein
A;Residues: 1-6 <CON>
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R; Broom, M.F.; Mellor, D.M.; Chadwick, V.S.
Experientia 45, 1097-1099, 1989
A; Title: Purification and amino acid sequencing of naturally occurring N-formyl-met)
A; Reference number: A60986; MUID: 90092408; PMID: 2689204
A; Accession: A60986
A; Molecule type: protein
A; Residues: 1-6 < BRO>
C; Comment: This hexapeptide was the longest of several N-formyl oligopeptides report
F; 1/Modified site: N-formylmethionine #status experimental
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C;Species: Escherichia coli
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.1%; Score 9; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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                                                                                                                                                                                    A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistoscma mansoni) (fragm C;Species: Schistoscma mansoni
C;Species: Schistoscma mansoni
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C;Accession: A37114
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
R;Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
A;Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistoscma mansoni. Furt A;Reference number: A37114; MUID:90337955; PMID:2199439
A;Reference number: A37114
A;Re
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H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C; Species: Leuconostoc oenos phage P32
C; Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C; Accession: H44817
J. Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A; Title: Lysogeny in Leuconostoc oenos.
A; Reference number: A44817; MUID: 92085033; PMID: 1748868
A; Accession: H44817
A; Molecule type: protein
A; Residues: 1-5 < ARE>
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F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C;Species: Leuconostoc oenos phage P54
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: F44817
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUD:92085033; PMID:1748868
A;Accession: F44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
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cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrior C; Species: mitochondrion Lampetra fluviatilis (river lamprey)
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: T13892
R; Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A; Title: The main features of the craniate mitochondrial DNA between the NDI and t A; Reference number: Z17775; MUD: 97398704; PMID: 9254918
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(Species: Salmonella typhimurium
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the c
A;Accession: E60274
A;Accession: E60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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A;Molecule type: DNA
A;Residues: 1-3 <DEL>
A;Residues: 1-3 <DEL>
A;Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123
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C;Keywords: mitochondrion; oxidoreductase
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-5 <VOG>
A, Cross-references: GB: M62408
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C; Accession: E30608
R; Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Sold
J. Immunol. 142, 3158-3163, 1989
A; Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A; Reference number: A30601; MUID:89215279; PMID:2496160
A; Reference number: A30601; MUID:89215279; PMID:2496160
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 < GON>
C; Keywords: heterotetramer; immunoglobulin
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                                                              C; Species: Leuconostoco cenos phage PZI11-15
C; Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C; Accession: B44817
R; Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, Z135-2139, 1991
A; Title: Lysogeny in Leuconostoc cenos.
A; Reference number: A44817; MUID:92085033; PMID:1748868
A; Accession: B44817
A; Molecule type: protein
A; Residues: 1-5 < ARE>
A; Note: sequence extracted from NCBI backbone (NCBIP:70342)
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D44817
35K structural protein - Leuconostoc oenos phage PAt5-12 (fragment)
C;Species: Leuconostoc oenos phage PAt5-12
C;Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C;Accession: D44817
C;A
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                                      structural protein - Leuconostoc oenos phage PZt11-15 (fragment)
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

1, 2004, 10:56:46; Search time 11.6667 Seconds
 (without alignments)
57.715 Million cell updates/sec June Run on:

US-09-712-819C-1 32 1 FTLTISS 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

457 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

	Description	branched-chain-ami	T-cell receptor be	4.5K structure	5K structural	Ig kappa chain V-I	ဝ	lar pro	major protein anti	hypoxanthine phosp	34.5K structural p	tructural	e protein t	М	parasporal crystal	8K ubiqui	Y protein - human	12-I	pilE protein - Esc	heromone o	sex pheromone cCF1	18K protein 5507 -	9	21	l recer	T-cell receptor be	T-cell receptor be	-cell	Ö	T-cell receptor be
SUMMAKIES	ID	A40135	PT0644	B44817	D44817	090	T13892	236	E60274	A37114	H44817	F44817	869237	609	S14159	\sim	137263	I65546	S25266	A25269	A30812	PS0254	PN0649	309066	C)	an.	PT0645	71	0	
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T-cell receptor be glycogen phosphory biotin B - Citroba		hypothetical prote myosin light chain Ig heavy chain CRD	T-cell receptor be T-cell receptor be T-cell receptor be T-cell receptor be	T-cell receptor be T-cell receptor be T-cell receptor be
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30 31 35	33 34 55	36 337 38	3 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 ይ 4 3

ALIGNMENTS

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A40135
branched-chain-amino-acid transaminase (BC 2.6.1.42), mitochondrial - rat (fragment
N;Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial
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                                                                     C.Species: Rattus norvegicus (Norway rat)
C.Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 30-Sep-1993
C.Accession: A40135
R.Hutson, S.M.; Wallin, R.; Hall, T.R.
submitted to the Protein Sequence Database, March 1992
A.Reference number: A40135
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-4 <HUT>
C; Keywords: aminotransferase; mitochondrion
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RESULT 2

A. Status: translation not shown
A. Status: translation not shown
A. Residues: 1-5 < FEE>
A. Residues: 1-5 < FEE> T-cell receptor beta chain V-D-J region (111-1G) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997 C, Accession: PT0644

A, Experimental source: newborn thymus, strain BALB/c C; Keywords: T-cell receptor

. 0 Query Match 34.4%; Score 11; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels

. 0

Gaps

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RESULT 3

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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 11:18:42; Search time 34.6667 Seconds

(without alignments)
56.387 Million cell updates/sec

Perfect score: 33
Sequence: 1 FTLKISR 7
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 49082

Minimum DB seq length: 0
Maximum Match 1008
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 198, App	Sequence 7, Appli	Sequence 205, App	Sequence 370, App	Sequence 145, App	Sequence 145, App	Sequence 105, App	Sequence 131, App	Sequence 460, App	Sequence 164, App	Sequence 164, App	Sequence 78, Appl	Sequence 164, App	Sequence 39, Appl	Sequence 30, Appl
	ID	US-09-791-378-198	US-09-998-909-7	US-09-826-290-205	US-09-826-290-370	US-09-791-393-145	US-09-791-389-145	US-10-601-100-105	US-10-264-309-131	US-10-264-309-460	US-09-996-288-164	US-09-996-265-164	US-10-162-497-78	US-10-461-863-164	US-10-105-930-39	US-10-043-539-30
	DB	. 6	σ	0	σ	10	10	12	16	16	σ	10	14	15	14	14
	Query Match Length DB	7	7	7	7	2	7	7	7	7	7	7	7	7	G	w
οķο	Query Match	60.6	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	54.5	54.5	54.5	54.5	51.5	51.5
	Score	20	20	20	20	20	20	20	20	20	18	18	18	18	17	17
	Result No.		7	m	4	Ŋ	9	7	60	თ	10	11	12	13	14	15

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-10-020-354-10 09-996-288-135 -09-996-265-13 -10-044-034-13	5 US-10-461-863- US-09-727-963A- 4 US-10-211-994- 4 US-10-020-354-	9 US-09-989-789-1396 9 US-09-989-789-1971 9 US-09-989-789-3503 9 US-09-989-789-3544 9 US-09-989-789-3544	US-09-796-848A US-09-844-508- US-09-808-387- US-09-996-288-	US- US- OSD OSD OSD	0 US-09-990-186-3 0 US-09-990-186-3 0 US-09-996-265-3 0 US-09-996-265-9 0 US-09-996-265-1 0 US-09-989-994-3 0 US-09-989-994-3 0 US-09-989-994-3
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0 C 8 C C	0400	2 2 2 2 2 2 4 4 5 5 5 5 5 5 5 5 5 5 5 5	. 6 6 6 6	20000000000000000000000000000000000000	

ALIGNMENTS

RESULT 1 US-09-791-378-198

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Sequence 199, Application US/09791378

Sequence 199, Application US/09791378

Parent No. US2020142303A1

GENERAL INFORMATION:

APPLICANT: Parekh, Rajesh

TITLE OF INVERTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVERTION: SCHIZOPHENDA.

FILE REPERENCE: 9195-061-999

CURRENT APPLICATION NUMBER: US/9791,378

FRIOR APPLICATION NUMBER: US/9791,378

CURRENT APPLICATION NUMBER: US/9791,378

SOFTWARE: PATOR PLANTO DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 677

SOFTWARE: PATOR PROTEIN OF US/9791,378

CURRENT APPLICATION US/9791, Dred. NO'. 14+06;

MATCHES 3; COMBERTALY

OUG-TY MATCH

BEST LOCAL SIMILATITY 42.94; Pred. NO'. 14+06;

MATCHES 3; COMBERTALY

OY 1 FTLKISR 7

SEGUENC 7, APPLICATION US/09998909

PATOR NUMBER OF US/200014464A1

SEGUENC 7, APPLICATION US/09998909

PATOR NUMBER OF US/200014464A1

SEGUENCE AT NUMBER UNFORMATION:

APPLICANT: Havary, John

TITLE OF INVERTION: Detection and Treatment of Prostate Cancer
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type: PRT CAGANISM: homo sapien US-09-791-393-145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: homo sapien
US-09-826-290-370
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1 YTFELSR 7
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US-09-791-393-145
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Sequence 205, Application US/09826290

APPLICANT: Friedman, David L.

APPLICANT: Friedman, David L.

APPLICANT: Friedman, David M.

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Potter, David M.

APPLICANT: Potter, David M.

APPLICANT: Stiber; B. Michael

APPLICANT: Stiger, Thomas R.

APPLICANT: Williams Robert Reid

APPLICANT: Williams, Stephen A.

TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treat

TITLE OF INVENTION: Alzheimer's Disease

FILE REFERENCE: 2572-1-001 N2

CURRENT APPLICATION NUMBER: US 60/253,647

PRIOR APPLICATION NUMBER: US 60/253,647

PRIOR FILING DATE: 2000-04-03

PRIOR FILING DATE: 2000-04-03

PRIOR PELICATION NUMBER: US 60/253,647

PRIOR PELICATION NUMBER: US 60/253,647
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                        60.6%; Score 20; DB 9; Length 7; 42.9%; Pred. No. le+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo mapiens
US-09-998-909-7
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; ORGANISM: homo sapien
US-09-826-290-205
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1 FTFEYSR 7
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1 YTFELSR 7
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US-09-826-290-370
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Sequence 145, Application US/09791393
; Sequence 145, Application US/09791393
; Publication No. US20030032200A1
; GRENEAL INFORMATION:
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Rohlff, Christian
APPLICANTON: Diagnosis and Treatment of Bipolar Affective Disorder
AFILE OF INVENTION: and Unipolar Depression
ATILE OF INVENTION: and Unipolar Depression
ATILE OF INVENTION: and Unipolar Depression
ATILE OF INVENTION NUMBER: US/09/791,393
CURRENT FILING DATE: 2000-02-24
EARLIER FILING DATE: 2000-02-24
EARLIER FILING DATE: 2000-12-08
EARLIER FILING DATE: 2000-12-08
EARLIER FILING DATE: 2000-12-08
EARLIER FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SEQ ID NO 145
LENGTH: 7
LENGTH: 7
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APPLICANT: Friedman, David L.
APPLICANT: Herath Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Ximmel, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Farekh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Rohlff, Christian
APPLICANT: Stiger, Thomas R.
APPLICANT: Stiger, Thomas R.
APPLICANT: Stiger, Thomas R.
APPLICANT: Sunderland, P. Trey
APPLICANT: White, Frost
APPLICANT: White, Frost
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity 42.9
Matches 3; Conservative
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR, TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE FILE REFERENCE: POA-002.01
CURRENT APPLICATION NUMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/326,708
PRIOR PILING DATE: 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                            APPLICANT: FORDAN, DAVID L.
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: FRIEDMAN, DAVID L.
APPLICANT: KIMMEL, LIDA H.
APPLICANT: ROHLEF, CHRISTIAN
APPLICANT: POTTER, DAVID M.
APPLICANT: SOTTER, DAVID M.
APPLICANT: STIBER, B. MICHAEL
APPLICANT: STIBER, PETER J.
APPLICANT: STIBER, PETER J.
APPLICANT: STIBER, PETER J.
APPLICANT: STIBER, THOMAS R.
APPLICANT: STIBER, THOMAS R.
APPLICANT: STIBER, THOMAS R.
APPLICANT: STIBER, THOMAS R.
APPLICANT: WHITE, W. FROST
APPLICANT: MILLIAMS, STEPHEN A.
TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISE
TITLE OF INVENTION: UNMBER: US/10/264,309
CURRENT FILING DATE: 2002-10-03
PRIOR PPLICATION NUMBER: 60/326,708
PRIOR PPLICATION NUMBER: 60/326,708
PRIOR PPLICATION NUMBER: 60/326,708
PRIOR PPLICATION NUMBER: 60/326,708
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; Sequence 131, Application US/10264309; Publication No. US20040022794A1; GENERAL INFORMATION:
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ROHLFF, CHRISTIAN
SILBER, B. MICHAEL
SNYDER, PETER J.
SOARES, HOLLY D.
STIGER, THOMAS R.
SUNDERLAND, P. TREY
TOWNSEND, ROBERT R.
WHITE, W. FROST
WILLIAMS, STEPHEN A.
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ND. P. TREY
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SOFTWARE: PatentIn Version 2.1
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-131
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1 FTFBYSR 7
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US-10-264-309-460
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Sequence 164, Application US/10461863
Sequence 164, Application US/10461863
Sequence 164, Application US/10461863
GENERAL INFORMATION:
APPLICANT: Oliver, Cynthia
APPLICANT: Allan, Christian
APPLICANT: Chang, Stephen
TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORM
TILE REFERENCE: 10271-071-999
CURRENT APPLICATION NUMBER: US/10/461,863
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/388,920
PRIOR FILING DATE: 2002-06-14
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                                                                                                                                                                                                                                            ### FULLICATION NO. US20030158398A1

GENERAL INFORMATION:

APPLICANT: Chen, H.

APPLICANT: Freimer, N.

TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS

TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS

FILE REFERENCE: 7653-139

CURRENT APPLICATION NUMBER: US/10/162,497

CURRENT FILING DATE: 2002-06-04

PRIOR APPLICATION NUMBER: US/09/657,474

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-28

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-0-05

PRIOR FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SCOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 78
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SOFTWARE: Patentin version 3.1
SEQ ID NO 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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Matches 3; Conservative
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; ORGANISM: Homo sapiens
US-10-162-497-78
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CORGANISM: Homo sapiens
US-10-461-863-164
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2 YTMKYS 7
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Sequence 164, 32

Sequence 164, 32

Patent No. US_0020177126A1

GENERAL INFORMATION:

APPLICANT: Young, James

APPLICANT: Scott, Koenig

APPLICANT: Leslie, Johnson

TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi

TITLE OF INVENTION: and Treatment

FILE REFERENCE: 10271-047-999

CURRENT APPLICATION NUMBER: US/09/996,288

CURRENT FILING DATE: 2001-11-28

NUMBER OF SEQ ID NOS: 259

SOFTWARE: PatentIn version 3.1

SEQ ID NO 164

LENGTH: 7
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Sequence 164, Application US/09996265

Sequence 164, Application US/09996265

Sequence 164, Application US/09996265

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
TITLE O
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le+06;
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Pred. No. 1e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                               Score 20; DB :
Pred. No. 1e+00
3; Mismatches
SOFTWARE: Patentin Version 2.1 SEQ ID NO 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.5%;
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Best Local Similarity 42.9%;
Matches 3; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-309-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT CORGANISM: Homo sapiens US-09-996-288-164
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CORGANISM: Homo sapiens
US-09-996-265-164
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Best Local Similarity
Matches 3; Conserv
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1 YTFELSR 7
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US-09-996-288-164
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US-09-996-265-164
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Sequence 30, Application US/10043539

Sequence 30, Application US/20030114650A1

GENERAL INFORMATION:
APPLICANT: Cheung, Ambrose

APPLICANT: Zhang, Gongyi

TITLE OF INVENTION: BACTERIA

FILE OF INVENTION: BACTERIA

FILE REFERENCE: DC-0199

CURRENT FILING DATE: 2002-01-11

FRIOR PPLICATION NUMBER: US 60/261,233

PRIOR FILING DATE: 2001-01-12

PRIOR PPLICATION NUMBER: US 60/261,607

PRIOR PLING DATE: 2001-01-12

PRIOR PLING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 2001-05-08

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.1

SEQ ID NO 30

LENGTH: 6
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                                                       RESULT 14
US-105-930-39

Sequence 39, Application US/10105930

Publication No. US20030009018A1

GENERAL INFORMATION:

APPLICANT: Maeda, Masatsugu

APPLICANT: Waguchi, No. US20030009018A1iko

TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN,

FILE REFERENCE: 06501-105US1

CURRENT APPLICATION NUMBER: US/10/105,930

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER: JP 2000-240397

PRIOR PILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-27

NUMBER OF SEQ ID NOS: 77

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 39

LEMOTH: 6

LEMOTH: 6
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Pred. No. 1e+06;
2; Mismatches
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CRGANISM: Staphylococcus aureus
US-10-043-539-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 3, Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Homo sapiens
US-10-105-930-39
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us-09-712-819c-6.closed.rai

36, Appl 53, Appl 55, Appl 17, Appl 17, Appl 26, Appl 62, Appl 41, Appl 41, Appl 61, Appl 41, Appl 41, Appl

Sequence Sequence Sequence

Sequence

Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence

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APPLICANT: Lichenstein, Henri
APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 1; Length 7;
Pred. No. 3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.

ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
US-08-305-871A-17

US-08-788-822A-1

US-08-134-231C-36

US-08-728-160-36

US-08-136-743B-63

US-08-591-632-17

US-08-591-632-17

US-08-591-632-17

US-08-591-632-17

US-09-611-451-17

US-09-611-451-17

US-08-136-743B-62

US-08-136-743B-62
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PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:
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CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.1
Matches 4; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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396, App
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                                                                                                                                          June 1, 2004, 11:13:51; Search time 13.6667 Seconds (without alignments) 26.443 Million cell updates/sec
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Sequence 78
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Sequence 3
Sequence 7
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'cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
'cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-346-333-24
US-08-346-333-24
US-09-268-992-78
US-09-657-474-78
US-08-173-750B-20
PCT-US-174-060-17
US-08-174-060-17
US-08-18-18-18-18
US-08-591-632-23
US-08-591-632-23
US-09-611-451-23
US-09-989-789-354
US-09-989-789-3542
US-09-989-789-3542
US-09-989-789-3542
US-09-989-789-3542
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PCT-US95-04075-8
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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33
1 FTLKISR 7
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Match Length
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                                                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                     OM protein
                                                                                                                                                                                                                                                                              Sequence:
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Gaps

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2 TLKI 5
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Fatent No. 5677153
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Palzkill, Timothy
TITLE OF INVENTION: Methods for modifying DNA and for
TITLE OF INVENTION: detecting effects of such modification on interaction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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APPLICANT: FAULDS, DARYL, VISHOOT, MIMI, BROOKS, EMILY
TITLE OF INVENTION: MYCOPLASMA HYOPNEUMONIAE ANTIGEN AND USES
APPLICANT: AMGEN INC.

TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like TITLE OF INVENTION: Protein NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC CITY: Thousand Oaks STREET: 1840 DeHavilland Drive CITY: Thousand Oaks STATE: California COUNTRY: U.S.
ZIP: 91320-1789
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TTLESTATION acids
TTLESTATION acids
TTLESTATION acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20; DB 5; Length 7; Pred. No. 3e+05; 1; Mismatches 2; Indels
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80.0%; Pred. No. 3e+05;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/335,726
FILING DATE: 07-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 30,130
FILING DATE: 26-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.1%;
Matches 4; Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: unk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 FTLKISR 7
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1 FTFEYSR 7
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US-08-346-333-24
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEREFORE
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WINTER OF INVERTOR: encoded modified polypeptides with targer substrates.

WORSENDERGREAR PROGRAMMENT ST.

CORRESCRATE RELABER FORM:

STREET A BABACHER OF TREGETION

STREET A BABACHER OF TREGET ST.

COUNTRY: 103 APRILOZION THE STREET STREET
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PET-011 (September 24, Application PC/TUS9107506)

Sequence 24, Application PC/TUS9107506

Senence 24, Application PC/TUS9107506

GENERAL INFORMATION:

APPLICANT: Botstein, David

APPLICANT: Palzkill, Timothy

TITLE OF INVENTION: Methods for modifying DNA and for

TITLE OF INVENTION: Methods for modified polypeptides with target substrates.

TITLE OF INVENTION: encoded modified polypeptides with target substrates.

TITLE OF INVENTION: Methods for modified polypeptides with target substrates.

TORRESPONDENCE ADDRESS:

ADDRESSEE: Richard F. Trecartin

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA
                                                                                                                           Gaps
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                                                                          Score 18; DB 4; Length 7; Pred. No. 3e+05; 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07506
FILING DATE: 19911021
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: FP-53469-PC/RFT
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: linear
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US-09-174-060-17
; Sequence 17, Application US/09174060
; Patent No. 5989554
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knuth, Mark W
APPLICANT: Haak-Frendscho, Mary
APPLICANT: Shultz, John W
APPLICANT: Lesley, Scott A
APPLICANT: Villars, Catherine E
                                                                        Query Match
Best Local Similarity 60.0%;
Matches 3; Conservative
     ; ORGANISM: Escherichia coli
US-08-753-750B-20
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MOLECULE TYPE: peptide
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Patent No. 6610506

GENERAL INFORMATION:

APPLICANT: Lo, Reggie Y.C.

APPLICANT: Schryvers, Anthony B.

APPLICANT: Schryvers, Andrew A.

TITLE OF INVENTION: FASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME FILE REFERENCE: A34762 021645.0105

CURRENT APPLICATION NUMBER: US/08/753,750B

CURRENT APPLICATION NUMBER: C2,164,274

PRIOR APPLICATION NUMBER: 60/008,569

PRIOR PILING DATE: 1995-12-01

PRIOR PILING DATE: 1995-12-01

PRIOR PILING DATE: 1995-12-01

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 7

TYPE: PRT
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US-09-657-474-78

Sequence 78, Application US/09657474

Patent No. 6399762

Patent No. 6399762

APPLICANT: No. 6399763

APPLICANT: Freimer, N.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: MUMBER: US/09/657,474

CURRENT APPLICATION NUMBER: US/09/657,474

PRIOR FILING DATE: 1999-03-16

PRIOR APPLICATION NUMBER: 09/236,134

PRIOR APPLICATION NUMBER: 00/106,056

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-03-16

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 1
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                                                                    DB 4; Length 7; 3e+05;
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Pred. No. 3e+05;
2; Mismatches 1; Indels
                                                                  Query Match 54.5%; Score 18; DB Best Local Similarity 50.0%; Pred. No. 3e+0 Matches 3; Conservative 2; Mismatches
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50.0%;
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Best Local Similarity 50.v
And 3; Conservative
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; ORGANISM: Homo sapiens
US-09-657-474-78
; ORGANISM: Homo sapiens
US-09-268-992-78
                                                                                                                                                           1 FTLKIS 6
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2 YTMKYS 7
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RESULT 11
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
TITLE OF INVENTION: PURIFICATION OF PROTEINS, PEPTIDES AND CONJUGATES FOR
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS: 25
ADDRESSEE: Ross & Stevens, S.C.
STREET: 1 South Pinckney St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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; Sequence 69, Application US/08654623
; Patent No. 6010884
; GENERAL INFORMATION:
    APPLICANT: Griffiths, Andrew D
; APPLICANT: Holliger, Kaspar-Philipp
    APPLICANT: Nissim, Ahuva
    APPLICANT: Winter, Gregory P
    TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; TITLE OF INVENTION: Recombinant Binding Proteins and Peptides
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6330 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.5%; Score 17; DB 2; Length 7; 75.0%; Pred. No. 3e+05; tive 1; Mismatches 0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/654,623
                                                                                                                                                                                      STATE: WI
COUNTRY: USA
ZIP: 53701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34506.024
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/338,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 34506
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-257-5353
TELEFAX: 608-257-9175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 608-25/-31/.
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.03
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-09-174-060-17
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STREET: 65.
CITY: Chicago
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Sequence 17, Application US/08338382
Patent No. 6069230
GENERAL INFORMATION:
APPLICANT: Knuth, Mark W
APPLICANT: Shultz, John W
APPLICANT: Shultz, John W
APPLICANT: Shultz, John W
APPLICANT: Uillars, Catherine E
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND FACILE
TITLE OF INVENTION: HIGH LEVEL EXPRESSION AND DETECTION APPLICATIONS
TITLE OF INVENTION: IMMUNIZATION, PURIFICATION AND DETECTION APPLICATIONS
NUMBER OF SEQUENCES:
ADDRESSEE: Ross & Stevens, S.C.
STREET: 1 South Pinckney St.
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Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels
      CLASSIFICATION: 435
CLASSIFICATION: (012N 1/21, C12R 1:19)
PRIOR APPLICATION: (012N 1/21, C12R 1:19)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9300816.7
FILING DATE: 16-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 93303614.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BP 93303614.7
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9412147.2
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9412147.2
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BCT/GB94/02662
FILING DATE: 05-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 20-JUN-1995
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: 28111/33259
FILING DATE: 05-DEC-1994
FILING DATE: 05-DEC-1994
PRIOR APPLICATION NUMBER: 36,107
FELEPHONE: (312) 474-6300
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARRACTERISTICS:
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARRACTERISTICS:
INFORMATION ACCIONS
INF
29-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 53701
COMPUTER READABLE FORM:
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1 SLKVS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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APPLICANT: Barbas, Carlos F.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: DESCRIPES REsearch Institute, Office of
ADDRESSEE: The Scripps Research Institute, Office of
CITY: La Jolla
STREET: 10550 NO. 6261558th Torrey Pines Road, TPC 8
COUNTRY: USA
ZIP: La Jolla
STREET: 1050 NO. 6261558th Torrey Pines Road, TPC 8
COUNTRY: USA
ZIP: 92037
COMPUTER: READABLE FORM:
NEDION TYPE: ROADATA:
COMPUTER: 19-COT-1994
PRIOR APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-COT-1994
PRIOR APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-COT-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-COT-1993
ATTORNEY/AGENT INFORMATION:
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COMPACTOR: TITE: FIGURY GIBN
COMPACTOR: TITE: FIGURY GIBN
COMPACE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles: 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 36.6.024
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity 75.0
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NAME: PRINCING TON NUMBER: 43.163

REPRENCE/COCKET NUMBER: 74.163

TELECOMORIO CACCET NUMBER: 7481 332.3

TYPE: anino esid of the caccet of
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us-09-712-819c-6.closed.rai

US-09-611-451-23

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| Sequence 44, Application US/08757425B
| Sequence 46, Application US/08757425B
| Patent No. 6500660
| GENERAL INFORMATION:
| APPLICANT: Fastrez, Jacques
| TITLE OF INVENTION: Chimeric Target Molecules Having A Regulatable Activity
| FILE REFREENCE: 100390-09640
| CURRENT APPLICATION NUMBER: US/08/757,425B
| CURRENT FILING DATE: 1996-11-27
| NUMBER OF SEQ ID NOS: 78
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 44
                                                                                       Gaps
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US-07-717-331F-5

Sequence S. Application US/07717331F

APPLICANT: Unue Nasrallah, Michael Masrallah; and Joshua APPLICANT: Unue Nasrallah, Michael Masrallah; and Joshua TITLE OF INVENTION: Encoded At The Self-Incompatability Locus CORRESPONDENCES:

ADDRESSER: Yahwak & Associates

CONTRY: Trumbull

STREET: 25 SKytop Drive

COUNTRY: USA

ZIP: Connecticut

COUNTRY: USA

ZIP: Connecticut

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy Disk

COMPUTER SYSTEM: MS-DOS

SOFTWARE: Macrosoft Word

CLASSIFICATION NUMBER: US/07/717,331F

FILING DATE: June 19th 1991

CLASSIFICATION NUMBER: 26,824

TELEDRANGE: (203) Z68-1951

TELEBRANG: (203) Z68-1951

TELEBRANG: (203) Z68-1951

TELEBRANG: (203) Z68-1951

TELEBRANG: Anino acid

TOPDICON: Hana
                                     Score 16; DB 4; Length 5;
Pred. No. 3e+05;
1; Mismatches 0; Indels
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                                                                                1; Mismatches
                                 48.5%;
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Matches 3; Conservative
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0; Gaps
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48.5%; Score 16; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 1; Indels
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Job time : 13.6667 secs
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mimetope
US-08-757-425B-44
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major fat-globule
hypothetical prote
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ribosomal protein
glycogen phosphory
phosphotransferase
18K protein 5507 -
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neuropeptide TB-6
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ribosomal protein
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51.795 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                   283366 seqs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: pir1: *
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Hatty-acid synthas MHC H2-L antigen - T-cell receptor be T-cell receptor be peptidyl-dipeptida choline oxidase (E pilE protein Esc sex pheromone cAM3 sex pheromone cCFl phosphonoacetaldeh omega-gliadine 1' Ig heavy chain CRD Ig kappa chain V-I T-cell receptor be peptidylglycine mo carnocin U149 - Ca		ext_change 13-Sep-1996 on site of muscle uridine diphosphogenghoprotein experimental lindels 0; Gaps 0;	
2 165546 2 PT0518 2 PT0518 2 AN0859 2 A25266 2 A25269 2 A25269 2 PT0269 2 PT0269 2 A38671 2 A38671	ALIGNMENTS	se (UDP-forming) (EC 2 s (domestic rabbit) evision 30-Oct-1992 #t e of the phosphorylati ; hexosyltransferase; ; Score 13; DB 2; I %; Pred. No. 2.8e+05; 0; Mismatches 0;	4.
		ucan-processing the state of th	
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glycoprotein component 16/major fat-globule membrane protein/MFG-EB homolog - bovine (freglycoprotein component 16/major fat-globule membrane protein/MFG-EB homolog - bovine (freglycoproteins: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Reference number: A48394
A;Accession: E48394
A;Accession: E4 Query Match 39.4%; Score 13; DB 2; Length 7; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 2; Conservative 2; Mismatches 0; Indels EISR 7 4 ò

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22K Superhelical DNA-binding protein - Escherichia coli (fragment)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61300
R;Kishi, F.; Ebina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982
A;Title: Purification and characterization of a protein from Escherichia coli which form A;Reference number: A61300; MUID:83082696; PMID:6294066
A;Rocession: A61300
A;Molecule type: protein
A;Residues: 1-4 <KIS>
C;Comment: This protein resembles some of the histone-like protein of bacteria in amino C;Keywords: DNA binding; monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Int. J. Syst. Bacteriol. 42, 144-150, 1992
A;Title: Electrophoretic heterogeneity of ribosomal protein AT-L30 among actinomycete ge
A;Reference number: S19630; MUID:92144363; PMID:1736962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0644
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Species: Streptomyces griseus
C,Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 06-Jun-1997
C,Accession: S19630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Score 11; DB 2; Le 100.0%; Pred. No. 2.8e+05; ive 0; Mismatches 0;
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A.Molecule type: mRNA
A.Residues: 1-5 <FEE>
A.Experimental source: newborn thymus, strain BALB/c
C.Keywords: T-cell receptor
Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 11; DB 2;
Pred. No. 2.8e+05;
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66.7%;
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Best Local Similarity 66.77
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Best Local Similarity 100.
Matches 2; Conservative
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A;Status: translatio
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                                                                                                                               DNA topoisomerase II alpha - Chinese hamster (fragment)
C; Species: Cricetulus griseus (Chinese hamster)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: 148086
R; Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
J. Biol. Chem. 270, 25850-25858, 1995
A; Title: Molecular cloning and characterization of the promoter for the Chinese hamster A; Reference number: 148086; MUID:96029684; PMID:7592770
A; Accession: 148086
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-7 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: B48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Petroselinum crispum (parsley)
Cispecies: Petroselinum crispum (parsley)
Cispecies: Petroselinum crispum (parsley)
Cidate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
CiAccession: T14910
Rikircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
Mol. Gen. Genet. 257, 595-605, 1998
A; Title: CPRF4d, a novel plant bZIP protein of the CPRF family: comparative analysis of A; Reference number: Z18261; MUID:98265918; PMID:9604882
A; Reference number: Z18261; MUID:98265918; PMID:9604882
A; Rocession: T14910
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-5 < KIR>
A; Experimental source: ssp. Hamburger Schnitt
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A;Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            major fat-globule membrane protein GP 55 - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 < MAT>
A; Experimental source: milk
A; Note: sequence extracted from NCBI backbone (NCBIP:131444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
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Best Local Similarity 50.0
Matches 2; Conservative
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neuromodulatory peptide WWamide-2 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Decies: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the A;Reference number: S33244; MUID:93265912; PMID:8495720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (fragn C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol: 14, 807-813, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Describes: Achatina fulica (giant African snail)
C;Species: Achatina fulica (giant African snail)
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33244
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A;Reference number: S33244; MUID:93265912; PMID:8495720
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                                                                                                                                                                                                                                                           Length 7;
  submitted to JIPID, April 1993
A,Reference number: PS0206
A,Accession: PS0254
A;Molecule type: protein
A,Residues: 1-7 <TSU>
A,Experimental source: leaf, chloroplast, strain Nihonbare
A,Note: molecular weight 18K, pI 4.4
                                                                                                                                                                                                                                                         Query Match 30.3%; Score 10; DB 2; I Best Local Similarity 40.0%; Pred. No. 2.8e+05; Matches 2; Mismatches 1;
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A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-7 <MIN>
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A, Molecule type: protein
A, Residues: 1-7 <MIN>
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Best Local (
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T13892
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N; Alternate names: glycogen phosphorylase b C; Species: Liza ramada
C; Species: Liza ramada
C; Species: Liza ramada
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C; Accession: A60521
R; Bonamusa, L; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A; Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A; Reference number: A60521; MUID:90227907; PMID:2109669
A; Accession: A60521
A; Molecule type: protein
A; Residues: 1-5 <BON>
C; Superfamily: glucan phosphorylase
C; Keywords: glycosyltransferase; hexosyltransferase; phosphorylase b kinase) #status experim
F; 3/ Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase)
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C:Species: Escherichia coli
C:Species: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C;Accession: B39127
C;Accession: B39127
R;Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A;Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of
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C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C;Accession: P$0254
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A;Accession: B39127
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-7 <HAR>
A;Residues: 1-7 <HAR>
A;Cross-references: GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:g155144
C;Keywords: phosphotransferase
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C, Superfamily: Escherichia coli ribosomal protein L30
C, Keywords: protein biosynthesis; ribosome
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3 LKITQ 7
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5 QIS 7
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C; Species: Salmonella typhimurium
C; Species: Salmonella typhimurium
C; Species: Salmonella typhimurium
C; Species: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C; Accession: E42364
K; Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J; Bacteriol. 173, 3564-3572, 1991
A; Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq A; Reference number: A42364; MUID:91258342; PMID:1646201
A; Reference number: Pa2364
A; Reference number: Preliminary
A; Residues: 1-5 <VOG>A; Residues: 1-5 <VOG>A; Cross-references: GB:M62408
Title: The main features of the craniate mitochondrial DNA between the ND1 and the COIRE Reference number: Z17775; MUID:97398704; PMID:9254918

Accession: T13892

Accession: T13892

Status: preliminary; translated from GB/EMBL/DDBJ

Molecule type: DNA

Residues: 1-3 < DEL>

Cross-references: EMBL:Y09528; NID:g2340016; PIDN:CAA70721.1; PID:g4379123

Genetics:
Geneme: mitochondrion

NOte: COI

Note: COI
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27.3%; Score 9; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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27.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+D5;
Matches 2; Conservative 0; Mismatches 0; Indels
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Job time : 14 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 2, 2004, 18:47:58 ; Search time 10 Seconds (without alignments) 36.449 Million cell updates/sec

US-09-712-819D-12 33 1 FTLEISR 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_42:* Database :

SUMMARIES

Description	91	2072 lito	82073 litori	2101 litoria	5919 8	H H	P38639 mus musculu	0104 ente	P16101 alcaligenes	P11932 enterococcu	Φ	3698	P81817 carcinus ma	5826	80628	818	œ	P81807 carcinus ma	81808	8215	31889 ascari	82071	25154 oryctola	41491	31890 ascari	P38641 mus musculu	P35920 achatina fu	P35904 achatina fu	42562	2563	58705 anthopl	42561	œ
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Gaps . 0 Query Match 39.4%; Score 13; DB 1; Length 6; Best Local Similarity 75.0%; Pred. No. 1.4e+05; Matches 3; Conservative 0; Mismatches 1; Indels

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2 TLEI 5 3 TAEI 6 ਨੇ 日 RESULT 2
RE31_LITRU
AC 982072;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rubellidin 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryadinae; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NOEL TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RA TISSUE=Skin secretion;
RA TISSUE=Skin secretion;
RA TISSUE=Skin secretion;
RA TISSUE ST., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., RA TIPS tructure of new peptides from the Australin red tree frog
RT 'Litoria rubella'. The skin peptide profile as' a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).

TISSUE-Skin secretion;
TISSUE-Skin secretion;
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
"The structure of new peptides from the Australin red tree frog
'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians.";
Aust. J. Chem. 49:955-963(1996).

Query Match

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Gaps

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Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NGBI TaxID=6530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Achatina fulica (Giant African snail).
Bukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBI_TaxID=6530;
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MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., Ikeda T., muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
-!- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.
PIR; $33245; $33245.
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MEDLINE-93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi.M., Nomoto K.;
"WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
Litori electrica. Comparison with the skin peptides from Litoria
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                                                                                                                                                                                                                                               Query Match 30.3%; Score 10; DB 1; Length 7; Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
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7 AA; 993 MW; 7362D5B69B041310 CRC64;
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7 AA; 834 MW; 6DD05B076B0B5030 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
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01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                          rubella.";
Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
MOD RES 7 A MIDATIO
SEQUENCE 7 AA; 834 MW; 6DD05B076B
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P35921;
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ID WWAI ACHFU
AC P35919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skin secretion; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria
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TISSUE=Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rubellidin 3.2.

Rubellidin 3.2.

Rubellidin 3.2.

Rubellidin 3.2.

Rubellidin 3.2.

Retazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae, Pelodryadinae, Litoria.

NCBL_TaxID=104895;
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Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aust. J. Chem. 52:639-645(1999).
-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
         -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
                                                                                                                                                                                                                                                                                                               ;
0
                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
-!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
Amphibian defense peptide; Amidation.
MOD_RES 5 AMIDATION.
SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
Amphibian defense peptide.
SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
                                                                                                                                                                                                                                                    Match 33.3%; Score 11; DB 1; Length 5; Local Similarity 100.0%; Pred. No. 1.4e+05; es 2; Conservative 0; Mismatches 0; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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Last annotation update)
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28-FEB-2003 (Rel. 41, Last seque
10-OCT-2003 (Rel. 42, Last anno
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E105_LITRU
AC P82101;
DT 28-FEB-2003 (
DT 28-FEB-2003 (
DT 10-OCT-2003 (
DE E10-CT-2003 (
DE E10-CT-2003 (
C EUKARYOCA; MC
OC EUKARYOCA; MC
OC PRODING (
C MMPhibia; Bal
OC PRODING (
C MCBI TAXID=1(
R) SEQUENCE.
RC TISSUE=Skin |
RA Wabnitz P.A.
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AC P82073;
DT 28-FEB-2003
DC CC CC Amphibia; Ba
OC Amphibia; Ba
OC Amphibia; Ba
OC PELOTYAGINA
(1)
RP SEQUENCE:
RP Wabnitz P.A.
RT Litoria rube
RT Litoria; Ba
CC -!- FUNCTION
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent) (CIA).
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=81006769; PubMed=6997283;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
Identification and properties of the prosthetic group of choline oxidase from Alcaligenes sp.";
J. Biochem. 88:197-203(1980).
-1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=87005252; PubMed=3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
"Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAM373.";

FEBS Lett. 206:69-72(1986).

-!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
HARBORING PAM373.

-!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR SPECIFITY OF PHEROMONES TO PLASMIDS.

-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
PIR; A25269; A25269.

Pheromone.

SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alcaligenes sp.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 27.3%; Score 9; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 0; Mismatches 0; Indels
                                                                 Query Match 27.3%; Score 9; DB 1; Length 7; Best Local Similarity 100.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 0; Indelé
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          790 MW; 72C9D2C731B2C740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
Choline oxidase (EC 1.1.3.17) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AA.
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NCBI_TaxID=512;
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       7 AA;
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3 TL 4
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Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Blectrophoresis 15:735-745(1994).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown
protein is: 6.6, its MW is: 19 kDa.

NON TER
5 5
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SEQÜENCE 5 AA; 717 MW; 7364087043100000 CRC64;
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MEDLINE=89008313; PubMed=3139658;

Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Adsit J.C., Dunny G.M., Suzuki A.;

"Structure of cCF10, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline resistance plasmid, pCF10.";

J. Biol. Chem. 263:14574-14578 (1988).

-! FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1015.
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                                                                                               AMIDATION.
7362D5B69B132310 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AA.
FEBS Lett. 323:104-108(1993).
PIR, S33244; S33244.
Neuropeptide; Amidation.
MOD_RES 7 7 7 SEQUENCE 7 AA; 965 MW; 73
                                                                                                                                                                                  Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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       STRUK
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Query Match
Best Local Similarity 100.0
Matches 2; Conservative
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P81817;
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P58261:
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PSK_DAUCA
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Appl. Environ. Microbiol. 58:1417-1422(1992).
-!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
Active on Gram-positive bacteria.
Antibiotic; Bacteriocin; Lantibiotic.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and characterization of a new bacteriocin isolated from
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1998) to Swiss-Prot.
-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
cyclohydrolase I. This inhibition is reversed by L-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carnobacterium sp. (strain U149).
Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels
27.3%; Score 9; DB 1; Length 7; 66.7%; Pred. No. 1.4e+05; rative 0; Mismatches 1; Indels
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lantibiotic carnocin UI49 (Fragment).
                                                                                                                                                                                                                                        7 AA.
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-!- SUBUNIT: Homodimer (By similarity).
SWISS-2DPAGE; P99025; MOUSE.
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MEDLINE=92321768; PubMed=1622206;
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   Query Match
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                        GCHFR OR GFRP.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                          MOUSE
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicbtyledons, core eudicots, asterids, campanulids, Apiales, Apiaceae, Apioideae, Scandiceae, Daucinae,
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Phytogulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN=CV. US-Harumakigosun;

MEDLINE=20212743; PubMed=10750705;

Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,

Kamada H., Sakagami Y.,

"A secreted peptide growth factor, phytosulfokine, acting as a
stimulatory factor of carrot somatic embryo formation.";

Plant Cell Physiol. 41:27-32(2000).

-! FUNCTION: In presence of 2,4-D, stimulates proliferation of the
cells, but does not stimulate differentiation into the somatic
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Eur. J. Biochem. 250:727-734 (1997).
-!- FUNCTION: May act as a neurotransmitter or neuromodulator.
-!- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation; Multigene family.
MOD RES
S
SMIDATION (POTENTIAL).
SEQUENCE 5 AA: 586 MW; 672879D5AB300000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinus maenas (Common shore crab) (Green crab).

Bukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;

Bubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                     0; Indels
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27.3%; Score 9; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 24.2%; Score 8; DB 1; Length 5; Local Similarity 66.7%; Pred. No. 1.4e+05; es 2; Conservative 0; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Cerebral ganglion, and Thoracic ganglion; MEDLINE-98121193; PubMed-9461295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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TISSUE=Coleoptile;
TOUZET P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.1, its Mw is: 30.4 kba.
Maize-2DPAGE; P80628; COLEOPTILE.
Maize-DB; 123954; -. .
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Sulfation is important for activity and for the binding to a putative membrane receptor (By similarity).
-!- SIMILARITY: Belongs to the phytosulfokine family.
Growth factor; Sulfation.
PEPTIDE 1 4 SULFATION.
MOD_RES 3. 3 SULFATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 474)
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        PEPTIDE
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        PHYTOSULFOKINE-BETA.

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        5 AA; 687 MW; 76C1BBS04B300000 CRC64;

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Search completed: June 2, 2004, 18:58:22 Job time : 11 secs enterobacte nocardia la

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972081 nocardia de Q54248 streptomyce Q8kms9 enterobacte Q8kms9 enterobacte Q15897 homo sapien Q95945 saccharomyc P83533 lactobacill O50556 actinobacill O50553 arabidopsis Q8k3h6 rattus norv Q66113 cherry leaf O40564 fugu rubrip O08433 rattus sp. P83073 bacillus ce Q8kms3 klebsiella Du Q8g102 borrelia bu Q8g102 borrelia bu Q8g102 borrelia bu Q8g104 borrelia bu Q8g104 correlia vul
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STRAIN=DSM 20451;
DubMed=12112860;
Dress O., Weise W., Reil G., Parlar H., Wait R., Goerg A.;
Dress O., Weise step-wise altered protein expression in Lactobacillus sanfranciscensis.";
Proteomics 2:765-774(2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
PROTEIN IS: 15 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P83530;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBI TaxID=1625;
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P82181 spinacia ol
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Q721c0 caenorhabdi
O07354 sprechococo
P93233 lycopersico
Q8je81 human immun
P70804 azotobacter
Q15903 homo sapien
Q9yve3 human adeno
Q9yiq9 human adeno
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Q9yir0 human adeno
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                                                                                                                       June 2, 2004, 18:48:29; Search time 34.5 Seconds (without alignments) 64.018 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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P82181
P82182
Q7Z1C0
007354
P93233
Q87E81
P70804
Q15903
Q9YVE3
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
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Perfect score:
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6 AA; 675 MW; 6321B415B05DB000 CRC64;
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SEQUENCE FROM N.A.
STRAIN-Brigtol N2;
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SEQUENCE FROM N.A.
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Q7Z1C0
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                                                                                                                                                     TRAIN=CV. ALWARO; TISSUE=Leaf;

WEDLINE=20435798; PubMed=10874046;

WEDLINE=20435798; PubMed=10874046;

Yamaguchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 275.28466-28482(2000).

L. Siblian THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

-!- FUNCTION: THIS PROTEIN BILON THE CONTRICTLY TO 23S RIBOSOMAL RNA.

-!- FUNCTION: THIS PROTEIN BILON FAMILY OF RIBOSOMAL PROTEINS.

C. -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.

-!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.

GO; GO:0009507; C:chloroplast; IEA.

GO; GO:0003735; F:srnA binding; IEA.

GO; GO:0003735; F:structural constituent of ribosome; IEA.

RIDOSOMAL PROCEIN; Chloroplast; rRNA-binding.

RIDOSOMAL PROCEIN; Chloroplast; rRNA-binding.

RIDOSOMAL FER 6
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01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
NCBL_TaxID=3562;
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1e+06;
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01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 508 ribosomal protein L10 gamma (Fragment).
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Best Local Similarity
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Rhabditidae; Peloderinae; Caenorhabditis.
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Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
NCBI_TaxID=41431;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matode C. elegans: a platform for C. elegans Sequencing Consortium.";
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     Length 6;
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STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF043704; AAO38592.1; -.
Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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1e+06;
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39.4%; Score 13; DB 100.0%; Pred. No. 1e+tive 0; Mismatches
                                                                                                                                                                                                                                                                                                       Created)
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investigating biology. The C. elegar
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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MEDLINE=99069613; PubMed=9851916;
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0721C0;
01-OCT-2003 (TrEMBLrel. 25, Crea
01-OCT-2003 (TrEMBLrel. 25, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Hypothetical protein W01811.6.
                            ilarity 100.0%;
Conservative 0
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01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97351561; PubMed=9207843; Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; Differential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Lycopersicon esculentum)."; (Lycopersicon esculentum)."; Plant Mol. Biol. 34:275-286(1997).

EMBL; U75692; AAC49682.1; -. GO: GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA. GO; GO:0016829; F:lyase activity; IEA.
                                                              MEDLINE=99231861; PubMed=10217509; Huang T.C., Lin R.F., Chu M.K., Chen H.M.; "Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lycopersicon esculentum (Tomato).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                              0; Gaps
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
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                                                                                                                                                                             Microbiology 145:743-753(1999).
EMBL, AF003700, AAC35193.1; -.
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                         SEQUENCE FROM N.A.
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SEQÜENCE
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P93233
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STRAIN=4874;
MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; AF347267; AAK32344.1; -.
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Rehm B.H.A., Ertesvag H., Valla S.;
"A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.";
J. Bacteriol. 178:5884-5889(1996).
EMBL, X87973; CAA61230.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE FROM N.A.
TISSUE=Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                              Query Match 27.3%; Score 9; DB 15; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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O9YIRO;
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Q9YIRO
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Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,
                                                                                                                                                                                                                                                                                                                                                                        Human adenovirus type 7.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
VCBI_TaxID=10519;
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Virnses: dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99175282; PubMed=10074533; Crawford-Miksza L.K., Nang R.N., Schnurr D.P., Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease."; J. Clin. Microbiol. 37:1107-1112(1999).
             Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL; L32082; AAA73893.1; -.
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                                                                                                                                 Match 24.2%; Score 8; DB 4; Length 7; Local Similarity 50.0%; Pred. No. 1e+06; les 2; Conservative 0; Mismatches 2; Indels
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065065; AAD03662.1; ...
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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SEQÜENCE 7 AA; 849 MW; 6B040339CDD33DB0 CRC64;
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Q9Y1Q9;
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09Y1Q9
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Q9YVE3
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SEQUENCE FROM N.A.
MEDLINE=99099045; PubMed=9882359;
Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
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"Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a."; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF065064; AAD03659.1; -.
EMBL, AF065062; AAD03659.1; -.
EMBL, AF065063; AAD03659.1; -.
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MEDLINE=88078100; PubMed=2825819;
Rasschaert D., Gelfi J., Laude H.;
Rasschaert coronavirus TGEV: partial sequence of the genomic RNA its organization and expression.";
Biochimie 69:591-600(1987).
EMBL; AJ011482; CAA09625.1;
SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmissible gastroenteritis virus.
Viruses, ssRNA positive-strand viruses, no DNA stage, Nidovirales;
Coronaviridae, Coronavirus.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-CCT-2001 (TrEMBLrel. 18, Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical fusion protein.
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SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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Gallus gallus (Chicken).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauría, Aves; Neognathae, Galliformes, Phasianidae, Phasianinae,
Gallus.
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                                                  SEQUENCE FROM N.A.
STRAIN=KN T96-0620, S-1058, and CL 68578;
Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;
"Molecular surveillance of strain variation in adenoviruses causing acute respiratory disease, AV 4 and AV 7a.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF065068; AAD03668.1;
EMBL, AF065066; AAD03664.1;
EMBL, AF065066; AAD03666.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P83568;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pheromone peptide ILME.
Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepia.
Human adenovirus type 7a.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=Blood;
Wang Q., Li N., Li H.;
"Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF487519; AAL96665.1; -.
NON TER
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SEQUENCE 7 AA; 780 MW; 72CBIAB2D5BEBB70 CRC64;
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                                                                                                                                                                                                             Match 24.2%; Score 8; DB 12; Length 7; Local Similarity 33.3%; Pred. No. 1e+06; les 1; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                      Q8JJ20
Q8JJ20;
Q8JJ20;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Extracellular fatty acid binding protein (Fragment).
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SEQÜENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;
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Best Local Similarity
Matches 1; Conserv
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SPECTROMETRY
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P83568
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Q8JJ20
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RX Pubmed=1094467;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia RILME: a waterborne pheromonal peptide released by the eggs of Sepia RILME: a waterborne pheromonal peptide released by the eggs of Sepia RILME: Biochem. Biophys. Res. Commun. 275:217-222(2000).
RX PubMed=12207899;
RX Tatracting peptide.";
RY Pertilization in Sepia officinalis: the first mollusk sperm-RT attracting peptide.";
RY PERTILIZATION HAS WYOTROPIC ACTIVITY TARGETING THE GENITAL TRACT.
CC -1- SUBCELLULAR LOCATION SECRETED.
CC -1- SUBCELLULAR LOCATION SECRETED.
CC -1- TISSUE SECIFICITY: FOLLICE, FULL, GROWN COCYTE AND EGG(EC2).
CC -1- MASS SPECTROMETRY: WH=505.4; METHOD=MALDI.
CC -1- MASS SPECTROMETRY: WH=505.4; Pred. No. 1e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CM 3 LE 4

DD 3 ME 4

DD 3 ME 4

Search completed: June 2, 2004, 18:59:45
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Thu Jun

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2, 2004, 18:47:08; Search time 49 Seconds (without alignments) 40.364 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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33
1 FTLEISR 7
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Perfect score:
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                                                              OM protein
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                                                                                                                                                                                             Sequence:
                                                                                             Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A_Geneseq_29Jan04:* Database

Minimum DB seq length: 0 Maximum DB seq length: 7

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Adylege Rheumatoi Abb55870 Vascular Abb55881 Vascular Abb55981 Vascular Aau24969 Schizophr Aau26249 Depressio Aau15313 Schizophr Abb52190 Human API Abb52355 Human API Abb57355 Breast ca Abp57255 Breast ca Abb57203 Breast ca Abb57203 Breast ca Abb57203 Alzheimer Human afa Rheumatoi Vascular S4 deriva Scaffold Scaffold Staphyloc Staphyloc Staphyloc Abp57203 E Abr59010 A Abr59042 A Aay40736 S Aab30074 S Aab30076 8 Abr45678 9 Abr46070 8 Abr46070 8 Aar81848 SUMMARIES ABR45678 ABR46070 ABR46854 ABR59042 AAB30074 Length Query Match Result No.

Abr44950 Staphyloc	Abr46462 Staphyloc	Abr45342 Staphyloc	Aar07656 Ribonucle	Aay42013 Rheumatoi	Aaw82668 Cauliflow	Abu09135 Human int	80	U	Abr46238 Staphyloc	U)		Abr45454 Staphyloc	Aar72775 Mammalian	Aay40737 S4 deriva	Aay83858 Ribonucle	Aab30075 Scaffold	Aab47357 Cell lysi	Adb79629 Parapoxvi	Aaw84431 HIV-1 nuc
ABR44950	ABR46462	ABR45342	AAR07656	AAY42013	AAW82668	ABU09135	ABR45118	ABR45846	ABR46238	ABR46630	ABR47022	ABR45454	AAR72775	AAY40737	AAY83858	AAB30075	AAB47357	ADB79629	AAW84431
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human; afamin; serum protein family; albumin; alpha-foetoprotein; plasma; vitamin D binding protein; homology; post-translational processing; chromatography; Primer; PCR; amplification; probe; rheumatoid arthritis; ischaemia-reperfusion injury; ARDS; cardiopulmonary bypass; sepsis; toxic plasma substance; inflammation. Human afamin tryptic fragment FX20. Z AAR81848 standard; peptide; (first entry) 16-MAY-1996 AAR81848; RESULT 1 AAR81848

95WO-US004075 WO9527059-A1. Homo sapiens 31-MAR-1995; 12-OCT-1995

Wurfel MM, Wright Lichenstein HS, Lyons DE, WPI; 1995-358634/46

94US-00222619

31-MAR-1994;

(AMGE-) AMGEN INC. (UYRQ) UNIV ROCKEFELLER.

Human afamin or a variant and poly:nucleotide(s) encoding it - a human serum protein with activities in common with other members of this family.

Example 3; Page 45; 97pp; English.

Peptides AAR81847-54 are tryptic peptide fragments from human afamin (AAR81845) novel member of the human serum protein family. The fragments were used to design primers and probes (AAT00786-98) for the cloning of the afamin gene (AAT00785) from human liver cDNA. Afamin is thought to have similar properties to human albumin, alpha-foetoprotein and vitamin D binding protein due to homology with these proteins. The gene encodes a mature protein of 66576 daltons without post-translational processing (ca. 87000 daltons with post-translational processing isolated from human plasma by a conventional chromatographic methods. The

used in the exemplification of the present invention

Sequence 7 AA;

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A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample indicates the presence or expected or resting the abundance of an electrophoresis for the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to compounds that promote or inhibit their activity, which are then used as Compounds that promote or inhibit their activity, which are then used as compounds that promote or inhibit their activity, which are then used as compounds that promote or inhibit their activity, which are then used as protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAY42103 represent expression reference protein isoform peptides and AAZ425066 to AAZ25068 represent degenerate protein isoform peptides and AAZ425066 to AAZ25066 to AAZ25068 represent degenerate protein isoform also
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protein can be used to ameliorate ischaemia-reperfusion injury, rheumatoid arthritis, ARDS, cardiopulmonary bypass, sepsis, toxic plasma substances released after inflammation, etc
                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, rheumatoid arthritis, RA, diagnosis, RPI, RADF, detection, rheumatoid arthritis diagnostic feature, ERPI, synovial fluid, rheumatoid arthritis diagnostic protein isoform, screening; expression reference protein isoform, prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rheumatoid arthritis diagnostic protein isoform peptide #40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                      Query Match 72.7%; Score 24; DB 2; Length 7; Best Local Similarity 71.4%; Pred. No. 1.46+06; Matches 5; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    AAY41889 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-571871/48.
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                                                                                              Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                       Gaps
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                                                                                                                                                                                                                                                                                                                   Jascular dementia-associated protein isoform (VPI) 70.
72.7%; Score 24; DB 2; I
57.1%; Pred. No. 1.4e+06;
iive 2; Mismatches 1.
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                                                                                                                                                                                                                                                                                                                                                                            diagnosis; prognosis; gene therapy.
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                                                                                                                                                                                                      ABB55870 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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                                    4; Conservative
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Query Match
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Matches 4; Conserv
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                                                                                                WO200169261-A2.
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(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                                                                                                                                                                    VD; VD-associated protein isoform; VPI; screening;
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                                                                                                                                                                                                                  Vascular dementia-associated protein isoform (VPI) 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of VD and for gene therapy
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                                                                                                                                                                                                                                                                     diagnosis; prognosis; gene therapy.
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                                                                                                         ABB56283 standard; peptide; 7 AA
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24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSP) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                useful for
                                                                                 Vascular Dementia, VD, VD-associated protein isoform, VPI, screening, diagnosis, prognosis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, depression associated protein isoform, tryptic digest peptide, DPI, cerebrospinal fluid, CSF; BAD; bipolar affective disorder, neuropsychiatric disorder; bipolar mood disorder; neuroleptic; maniac-depressive illness; schizoaffective disorder.
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                                                 Vascular dementia-associated protein isoform (VPI) 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 4; I
Pred. No. 1.4e+06;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                            Rohlff C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 33; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU28602 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPI tryptic digest peptide #199.
                                                                                                                                                                                                                                                                     15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
                                                                                                                                                                                                                                      14-MAR-2001; 2001WO-GB001106
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Best Local Similarity
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YTFELSR 7
                                                                                                                                                                     WO200169261-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7 AA;
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                                                                                                                                    Homo sapiens
                                                                                                                                                                                                       20-SEP-2001.
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Matches
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Tyson KL

Terrett JA,

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New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                   The sequence represents a schizophrenia-associ|ated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of schizophrenia. The sequences can be used for treatment and diagnosis of schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as a nucleic acid probe to detect the presence of nucleic acids or SPIs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 4; Length 7;
Pred. No. 1.4e+06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                          Disclosure; Page 32; 148pp; English.
                                   (OXFO-) OXFORD GLYCOSCIENCES UK LID.
                                                                     Rohlff C,
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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28-DEC-2000; 2000US-00750395
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                                                                     Parekh RB,
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                                                                                                              WPI; 2001-570624/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
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                                                                        Herath HMAC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), maniac-depressive illnesses, attention deficit disorders. Sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
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                                                                                                                                                                                                                                                                                     Tyson KL
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 34; 153pp; English.
                                                                                                                                                                                                                                                                                          Rohlff C,
                                                                                                                                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD
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                                                                                                                                                                            24-FEB-2000; 2000GB-00004412.
08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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                                                                  WO200162787-A1
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                               Homo sapiens
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                                                                                                                                                                                                                                                 Human; Bipolar Affective Disorder; BAD; Depression-Associated feature; DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid; CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder; unipolar affective disorder.
                                                                                                                                                                                               Depression-Associated Protein isoform DPI-208.
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AAU26249 standard; peptide; 7 AA.
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RESULT 7 AAU24969

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The invention relates to a preparation comprising an isolated Bipolar Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are used to screen, diagnose or prognose of BAD or unipolar depression, identify a subject at risk of developing BAD or unipolar depression, or monitor the effect of therapy in a subject. They are also used to screen for or identify agents that interact with a DPI. These agents, antibodies against the DPIs, and nucleic acids encoding the DPIs are used to treat or prevent BAD or unipolar depression. Diseases that can be treated are attention deficient disorder, a schizoaffective disorder, a bipolar or a unipolar affective disorder. The DPIs are used in proteomics. The proteomic approach of using DPIs for screening, diagnosis or prognosis of proteomic approach of using DPIs for screening, diagnosis or prognosis of expression analysis, such as not being able to obtain central nervous system (CNS) tissue from a living patient under normal circumstances. The present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subjects having BAD
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Sequence 7 AA;

Gaps ; 0 Score 24; DB 4; Length 7; Pred. No. 1.4e+06; 2; Mismatches 1; Indels 72.7%; 57.1%; Query Match Best Local Similarity 57.1 Matches 4; Conservative

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AAU15313 standard; peptide; 7 AA. AAU15313;

24-OCT-2001 (first entry)

Schizophrenia-associated isoform peptide #198.

Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder; neurological disorder; neuropathy.

Homo sapiens.

WO200163293-A2

30-AUG-2001.

23-FEB-2001; 2001WO-GB000783

24-FEB-2000; 2000GB-00004415 28-DEC-2000; 2000US-00750395

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Parekh RB, Rohlff C; Herath HMAC,

WPI; 2001-502868/55.

Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.

Claim 6; Page 32; 160pp; English

The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of

The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or

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SCH and the relative abundance of at least 1 chosen feature correlates with the presence or absence of SCH, and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least 1 chosen feature which correlates with the severity of SCH. The expression and activity of the SFs, SPIs and related molecules (e.g. secondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes neuropsychiatric disorders such as SCH from neurological disorders, where manifestations of anatomical and biochemical changes have been identified in many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are necessary for improved treatment of neuropsychiatric disorders. AAUISI14-AAUISTAC represent the amino acid sequences of schizophrenia-associated in an and characterisation and characterisation of the secondary many cases the sequences of schizophrenia-associated and characterisation of the secondary many cases the amino acid sequences of schizophrenia-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, neuroprotective, nootropic, gene therapy, vaccine, Alzheimer's disease, Alzheimer's Disease-Associated Feature, AF, Alzheimer's Disease-Associated Protein Isoform, AFI, tryptic dig-Expression Reference Protein Isoform, ERPI, proteolysis.
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Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
Townsend RR, White F, Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     72.7%; Score 24; DB 4; Length 7; 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                             AAU15762 represent the amino acid sequences disoforms used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
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28-NOV-2000; 2000US-0253647P.
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Best Local Similarity 57.1
Matches 4; Conservative
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The invention relates to methods for the screening, diagnosis and prognosis of Alzheimer's disease. The methods involve the detection of Alzheimer's Disease-Associated Features (AFS) and Alzheimer's Disease-Associated Features (AFS) and Alzheimer's Disease-Associated Protein Isoforms (APIS) in cerebrospinal fluid, serum or Expression Reference Protein Isoform (ERPI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFS and APIS correlates with the produced from an API by proteolysis
plasma. The abundance of the AFs and APIs is then normalised to an Expression Reference Protein Isoform (ERPI) in order to determine whether a patient is suffering from, or has a predisposition to, Alzheimer's Disease. The relative abundance of the AFs and APIs correlates with the severity of Alzheimer's Disease. The present sequence is a peptide produced from an API by proteolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
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Alzheimer's disease, Alzheimer's Disease-Associated Feature, AF;
Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest,
Expression Reference Protein Isoform; ERPI; proteolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
Townsend RR, White F, Williams SA;
                                                                                                                                                            72.7%; Score 24; DB 4; Length 7; 71.4%; Pred. No. 1.4e+06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human API-125 tryptic digest peptide #8.
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28-NOV-2000; 2000US-0253647P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                  Similarity 71.4
5; Conservative
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                                                                                                                                                                                                                                      1 FTLEISR 7
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                                                                                                                              Sequence 7 AA;
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This invention relates to a novel method for screening or diagnosing multiple sclerosis (MS) in a subject to determine the stage or severity of MS, to identify a subject at risk of developing MS or to monitor the effect of a therapy administered. The method comprises analysing a sample body fluid from the subject by two-dimensional electrophoresis and correspond to spots identified on a 2D gel these proteins or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of the invention correspond to spots identified on a 2D gel these proteins may have antiinflammatory or neuroprotective activity. The methods of the invention and the compositions are useful for clinical screening.

CC may have antiinflammatory or neuroprotective activity. The methods of the invention and the compositions are useful for clinical screening.

CC diagnosis and treatment of MS, for monitoring the effectiveness of MS treatment, for selecting participants in clinical trials, for identifying creatment, for selecting participants in clinical trials, for identifying continuate the expression or activity of an MSPI are useful for treatment of MS. Agents that or development of MS, to prevent or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic condissing a sequence encoding an MSPI function by gene coids comprising are useful for promoting MSPI function by gene therapy. The present sequence represents a human multiple sclerosis therapy. The present tryptic digest peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening or diagnosing multiple sclerosis (MS), useful for e.g. determining the stage or severity of MS, comprises detecting the presence of MS-associated features or protein isoforms by 2-dimensional
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                                                                                                                                                                                                                                                                                                                 Multiple sclerosis associated feature (MSF) tryptic digest peptide #389.
                                                                                                                                                                                                                                                                                                                                                      Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF; human; multiple sclerosis-associated protein isoform; MSPI; antiinflammatory; neuroprotective.
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Pred. No. 1.4e+06;
2; Mismatches 1
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20-NOV-2001; 2001US-0331647P.
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Best Local Similarity 57.1
Matches 4; Conservative
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    Similarity 57.1
4; Conservative
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                                                                                                                                                                                                                                             ABG78901;
    Best Local
Matches
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DB 4; Length 7;

72.7%; Score 24;

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This invention relates to a novel method for screening or diagnosing multiple sclerosis (MS) in a subject to determine the stage or severity of MS, to identify a subject at risk of developing MS or to monitor the effect of a therapy administered. The method comprises analysing a sample body fluid from the subject by two-dimensional electrophoresis and detecting the presence of multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of the invention correspond to spots identified on a 2D gel these proteins may have antiinflammatory or neuroprotective activity. The methods of the invention and the compositions are useful for clinical screening, convention and the compositions are useful for clinical screening, treatment, for selecting participants in clinical trials, for identifying treatment, for selecting participants in clinical trials, for identifying the screening and developing drugs for treatment of MS. Agents that modulate the expression or activity of an MSPI are useful for treating or delaying the onset or development of MS, to prevent or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic cacids comprising a sequence encoding an MSPI function by gene therapy. The present sequence represents a human multiple sclerosis associated feature tryptic digest peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening or diagnosing multiple sclerosis (MS), useful for e.g. determining the stage or severity of MS, comprises detecting the presence of MS-associated features or protein isoforms by 2-dimensional electrophoresis.
                                                                                                                                                                                                                                                    Multiple sclerosis associated feature (MSF) tryptic digest peptide #218.
                                                                                                                                                                                                                                                                                          Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF; human; multiple sclerosis-associated protein isoform; MSPI; antiinflammatory; neuroprotective.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herath HMAC, Parekh RB, Rohlff C;
                                                                                                                                    ABG78730 standard; peptide; 7 AA
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20-NOV-2001; 2001US-0331647P.
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The present sequence is that of a peptide fragment of a novel human 50.8 kb a prostate cancer-associated protein that has been identified as a highly effective marker for prostate cancer. The novel protein includes a polypeptide that is related to human serum vitamin D binding protein (VDBP, see ABP58017). The present peptide corresponds to amino acids 346-352 of this VDBP allele. It is one of a series of peptides (see ABP58005-16) that distinguish VDBP-related proteins from other proteins, or which may be characterised as binding specifically to an anti-VDBP antibody. VDBP-related proteins are detectable at a higher concentration in serum a healthy mammal and can therefore be used as prostate cancer markers. They permit the rapid detection, preferably before metastases occur, of prostate cancer. A target prostate cancer-associated protein may be detected using a labelled antibody capable of binding specifically to the protein. Prostate cancer-associated proteins, and nucleic acids encoding them, are also useful as targets for treating prostate cancer therapy indicators for monitoring the efficiency of prostate cancer therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing or treating prostrate cancer by detecting in a sample isolated from the individual the presence of prostate cancer-associated protein.
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                                                                                                                                                                                                                        Prostate cancer marker protein peptide fragment,
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                                                                                                           ABP58010 standard; peptide; 7 AA
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                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                            diagnosis; gene therapy
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Query Match 72.7%; Score 24; DB 5; Length 7; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 2; Mismatches 1; Indels

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The present invention describes a method for screening, diagnosing or determining the stage or severity of breast cancer, identifying a subject at risk of developing breast cancer, or monitoring the effect of therapy administered to a subject with breast cancer, by generating a two-dimensional array of features comprising breast cancer-associated features (BFS), or quantitatively detecting breast cancer-associated features (BFS), or quantitatively detecting breast cancer-associated compositions comprising; (a) a BFI; (b) a multipody capable of immunospecifically binding to one of the BFIS; (2) a pharmaceutical compositions comprising; (a) a BFI; or a fragment or derivative of the artibody, and a carrier; (a) screening for a fragment or derivative of the antibody, and a carrier; (b) the antibody of (1), or a fragment or derivative of the antibody, or an extraction or activity of one or more BFIS, a BFI fragments, a BFI fragment, a BFI-related or proteins; (4) screening for or identifying agence that modulate the expression or activity of one or more BFIS, a BFI fragment, a BFI-related collyptide, or BFI-fusion proteins; and (5) treating or preventing the collyptide, or BFI-fusion proteins; and (5) treating or preventing or breast cancer. BFIS have oytostatic activity and can be used for screening, diagnoshing or determining the stage or severity of breast cancer. The antibodies, BFIS, administered to a subject with breast cancer. The antibodies, BFIS, administered to a subject with breast cancer. The antibodies of the activity of one or more BFIS are usedful for treating or preventing breast cancer. Collone or more BFIS are usedful for treating or preventing breast cancer. When a secondated tryptic digest performed by which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Screening, diagnosing or determining the stage or severity of breast cancer, comprises analyzing and quantitatively detecting Breast Cancer-Associated Features or Breast Cancer-Associated Protein Isoforms in a biological sample.
                                                                                                             Breast cancer associated feature, BF, BPI, breast cancer, diagnosis, breast cancer associated protein isoform, cytostatic, gene therapy.
                                                                Breast cancer associated tryptic digest peptide SEQ ID NO:154.
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                                                                                                                                                                                                                                                                                                                                                                                            02-MAY-2001; 2001GB-00010790.
27-JUL-2001; 2001GB-00018385.
14-AUG-2001; 2001GB-00019791.
16-AUG-2001; 2001GB-00020045.
22-NOV-2001; 2001GB-00028062.
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                      16-APR-2003 (first entry)
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Search completed: June 2, 2004, 18:57:50 Job time : 51 secs
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Query Match 72.7%; Score 24; DB 6; Length 7; Best Local Similarity 57.1%; Pred. No. 1.4e+06; Matches 4; Conservative 2; Mismatches 1; Indels

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June 2, 2004, 18:59:52 , Search time 37.5 Seconds (without alignments) 52.517 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		-7 Sequence 7, Appli					Sequence 105,	Sequence 131,	Sequence 460,	Seguence 4, A	Sequence 6,		Sequence 6, 7	39	7 0000000000000000000000000000000000000
SUMMARIES	ID	US-09-791-378-198	US-09-998-909-7	US-09-826-290-205	US-09-826-290-370	US-09-791-393-145	US-09-791-389	US-10-601-10	US-10-264-309	US-10-264-309	US-10-050-552A-4	US-10-234-026	US-10-238-965-4	US-09-876-388-6	US-10-105-930-39	2 C00 C0C_01_0II
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14 US-10-288-340- 9 US-09-772-105-2 9 US-09-876-388-7 14 US-10-287-892- 14 US-10-288-340-	9 US-09-727-963A-3 12 US-10-328-953-4 12 US-10-367-580-3 12 US-10-367-593-3 12 US-10-367-594-3	12 US-10-367-654-31 12 US-10-367-658-31 14 US-10-06-869-63 14 US-10-006-869-63 14 US-10-006-869-65	5 US-10-395-032-65 5 US-10-395-032-65 US-09-734-417-12 1 US-09-829-495-77 2 US-10-396-678-5 4 US-10-006-869-63	14 US-10-00 14 US-10-00 15 US-10-39 15 US-10-39 15 US-10-39 15 US-10-39
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ALIGNMENTS

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Sequence 1985, Application US/09791378

Sequence 10520020142303A1

GENERAL INFORMATION:
APPLICANT: Parekh, Rajesh
TITLE OF INVENTION: SCHIZOPHRENIA
FILE REFERENCE: 9195-061-999
CURRENT APPLICATION NUMBER: 09/750,395

PRIOR PILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 677

SOFTWARE: Patentin version 3.0

SEQ ID NO 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 72.7%; Score 24; DB 9; Length 7; Best Local Similarity 57.1%; Pred. No. 1e+06; Matches 4; Conservative 2; Mismatches 1; Indels
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APPLICANT: Kimmel, Lida H.
APPLICANT: Rimmel, Lida H.
APPLICANT: Parekh, Rajesh Bhikhu
APPLICANT: Porter, David M.
APPLICANT: Potter, David M.
APPLICANT: Stilber, B. Michael
APPLICANT: White, Frost
APPLICANT: Williams, Stephen A.
ITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
ITLE OF INVENTION: Alzheimer's Disease
ITLE OF INVENTION: Alzheimer's Disease
ITLE REFERENCE: 2572-1-001 N2
CURRENT PLING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR APPLICATION NUMBER: 2000-11-28
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 370
LENGTH: 7
Friedman, David L.
Herath, Herath Mudiyanselage Athula Chandrasiri
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Publication No. US20030032200A1
GENERAL INFORMATION:
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; ORGANISM: homo sapien
US-09-826-290-370
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APPLICANT: Priedman, David L.
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
APPLICANT: Raimel, Lida H.
APPLICANT: Salesh, Rajesh Bhikhu
APPLICANT: Potter, David M.
APPLICANT: Soller, B. Michael
APPLICANT: Soller, B. Michael
APPLICANT: Stiger, Thomas R.
APPLICANT: Stiger, Thomas R.
APPLICANT: Stiger, Thomas R.
APPLICANT: Stiger, Income R.
APPLICANT: Stiger, Income R.
APPLICANT: White, Frost
APPLICANT: Worler, Carid Molecules, Polypeptides and
APPLICANT: Worler, Stephen A.
ITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
TITLE OF INVENTION: Uses Therefor, Us/09/826,290
CURRENT APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/194,504
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR APPLICATION NUMBER: US 60/253,647
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 492
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH:
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Pred. No. 1e+06;
0; Mismatches
FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09/998,909
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,284
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 205, Application US/09826290
Patent No. US20020164668A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.7%;
71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-998-909-7
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; ORGANISM: homo sapien
US-09-826-290-205
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US-09-826-290-370
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JENERAL INFORMATION:

JAPPLICANT: Herath Mudiyanselage Athula Chandrasiri

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Porekh, Rajesh Bhikhu

APPLICANT: Porekh, Rajesh Bhikhu

TITLE OF INVENTION: Proteins, Genes and Their Use for

TITLE OF INVENTION: and Unipolar Depression

TITLE OF INVENTION: and Unipolar Depression

FILE REFERENCE: 2543-1-001 NI

CURRENT APPLICATION NUMBER: US/09/791,393

CURRENT FILING DATE: 2002-01-02

EARLIER APPLICATION NUMBER: GB 0030050.9

EARLIER APPLICATION NUMBER: US 60/254,830

EARLIER FILING DATE: 2000-12-08

EARLIER FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 308

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 145

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APPLICANT: INNOGENETICS N.V.
TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of
TITLE OF INVENTION: Method in Seases
FILE REFERENCE: 11362.0038.NPUS01
CURRENT APPLICATION NUMBER: US/10/601,100
PRIOR PILING DATE: 2003-06-20
PRIOR FILING DATE: 2002-06-21
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patentin version 3.2
SEQ ID NO 105
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Sequence 105, Application US/10601100
Publication No. US20040072261A1
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Best Local Similarity 57.1
Matches 4; Conservative
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TYPE: PRT
ORGANISM: homo sapiens
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CRGANISM: homo sapien
US-09-791-389-145
1 YTFELSR 7
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1 YTFELSR 7
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US-09-876-388-6
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; OTHER INFORMATION: A conserved sequence between Region 2 in IL-22 and IL-10
US-10-050-552A-4
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; Publication No. US20030097679A1
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
APPLICANT: Mark William Davey
; APPLICANT: Mark William Davey
; APPLICANT: Marc Charles Ernest Van Montagu
TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001C1
; CURRENT APPLICATION NUMBER: US/10/234,026
; CURRENT FILING DATE: 1997-05-07
; PRIOR FILING DATE: 1997-05-07
; PRIOR FILING DATE: 1998-05-07
; PRIOR FILING DATE: 2000-02-15
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; Sequence 4, Application US/10050552A
; Publication No. US20020187512A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/317,937
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
                                                                                                                                                           Query Match 72.7%; Score 24; DB 16; Length 7; Best Local Similarity 57.1%; Pred. No. 1e+06; Matches 4; Conservative 2; Mismatches 1; Indels
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SOFTWARE: PatentIn Version 2.1
SEQ ID NO 460
1.RNGTH: 7
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ORGANISM: artificial sequence
                                                                 TYPE: PRT CRGANISM: Homo sapiens US-10-264-309-460
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; Sequence 6, Application US/09876388
; Patent No. US200200049153A1
; GENERAL INFORMATION:
; APPLICANT: Bridon, Dominique P.;
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Ezrin, Alan M.
; APPLICANT: Leblanc, Darren L.
; APPLICANT: St. Pierre, Serge
; TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES
; FILE REFERENCE: 50086201610
; CURRENT APPLICATION NUMBER: US/09/876,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10238965
; Sequence 4, Application US/10238965
; Publication No. US20040002586A1
; GENERAL INFORMATION:
; APPLICANT: Nagem, Ronaldo A.P.
; APPLICANT: Colau, Didier
; APPLICANT: Renauld, Jean-Christophe
; APPLICANT: Polikarpov, Igor
; TITLE OF INVENTION: Crystal Structure of Interleukin-22
; FILE REFERENCE: LUD-5722 US
; CURRENT APPLICATION NUMBER: US/10/238,965
; CURRENT FILING DATE: 2002-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-09-10
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
                                                                                                                                                                                                               60.6%; Score 20; DB 14; Length 7; 50.0%; Pred. No. 1e+06; 1ive 3; Mismatches 0; Indels
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, NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
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PRIOR APPLICATION NUMBER: 09/623,618
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/US00/13563
PRIOR FILING DATE: 2000-05-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: artificial sequence
                                                                                                         ; TYPE: PRT
; ORGANISM: Brassica oleracea
US-10-234-026-6
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Best Local Similarity 50.0
Matches 3; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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FEATURE:
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Sequence 6, Application US/10287892

Publication No. US20030108567A1

GENERAL INFORMATION:

APPLICANT: L'Archeveque, Benoit

APPLICANT: L'Archeveque, Benoit

APPLICANT: Holmes, Darren L.

APPLICANT: Holmes, Darren L.

APPLICANT: St. Pierre, Serge

TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)

FILE REFERENCE: 500862001612

CURRENT APPLICATION NUMBER: US/10/287,892
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US-09-876-388-6
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Sequence 39, Application US/10105930

Publication No. US2003009918A1

GENERAL INFORMATION:
APPLICANT: Maeda, Masatsugu
APPLICANT: Yaguchi, No. US20030009018A1iko
TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
FILE REFERENCE: 06501-105081
CURRENT PILING DATE: 2002-03-25
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: UF 2000-240397
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 1999-09-27
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                  54.5%; Score 18; DB 9; Length 6; 50.0%; Pred. No. 1e+06; 1; Indels 1; of Mismatches 1; Indels
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver: 2.1
SCOTTWARE: Patentin Ver: 2.1
SEQ ID NO 6
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CRGANISM: Homo sapiens
US-10-105-930-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
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1 YTLQI 5
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Сp 8

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Gaps
                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; COTHER INFORMATION: Peptide
US-10-287-892-6
                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                             Score 18; DB 14; Length 6;
Pred. No. 1e+06;
2; Mismatches 1; Indels
; PRIOR APPLICATION NUMBER: 09/657,332
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 2, 2004, 19:08:54 Job time: 37.5 secs
                                                                                                                                                                                                                                                                                                  54.5%;
                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0
Matches 3; Conservative
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Sequence
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; Sequence No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; AMGEN Center, Patent Operations/RRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.7%; Score 24; DB 1; Length 7; 71.4%; Pred. No. 3e+05; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 9130-1789

ZIP: 9130-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
FILING DATE:
US-09-522-433B-12
US-09-839-542B-636
US-09-839-542B-650
US-08-136-743B-29
US-08-136-743B-29
US-08-136-743B-33
US-08-136-743B-33
US-08-136-743B-34
US-08-136-743B-54
US-08-136-743B-56
US-08-136-743B-59
US-08-116-116-116
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PCT-US95-04075-8
; Sequence 8, Application PC/TUS9504075
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Amgen Center, Particles STREET: 1840 DeHavilland Dr CITY: Thousand Oaks STATE: California COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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            STRANDEDNESS:
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US-08-222-619-8
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                                                                                                                                                                        June 2, 2004, 18:56:07; Search time 15.5 Seconds (without alignments) 23.315 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8,
Sequence 51
Sequence 21
Sequence 55
Sequence 55
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Sequence 6
Sequence 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-423-468A-6
US-08-123-419-21
US-08-123-419-21
US-08-136-743B-55
US-08-136-743B-55
US-09-623-618B-6
US-09-653-618B-6
US-09-653-618B-7
US-09-046-216-55
US-09-046-216-55
US-09-046-216-55
US-09-046-216-55
US-09-136-743B-62
US-09-18-78-743B-62
US-09-18-78-743B-62
US-09-18-78-650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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33
1 FTLEISR 7
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Match Length
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Perfect score:
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No
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Gaps

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APPLICANT: AMGEN INC.
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US95/04075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.6%; Score 19; DB 1; Length 6; 66.7%; Pred. No. 3e+05; tive 0; Mismatches 2; Indels
                                                                      APPLICANT: Lichenstein, Henri
APPLICANT: Lyons, David
APPLICANT: Lyons, David
APPLICANT: Wurfel, Mark
APPLICANT: Wright, Samuel
TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           STREET: 1840 DeHavilland Drive
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-04075-21
; Sequence 21, Application PC/TUS9504075
; GENERAL INFORMATION:
     Sequence 21, Application US/08222619
Patent No. 5652352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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Sequence 6, Application US/09423468A

Sequence 6, Application US/09423468A

Patent No. 6469149

GENERAL INFORMATION:

APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol

APPLICANT: Mark William Davey

APPLICANT: Description OF ASCORBIC ACID IN PLANTS

FILE REFERENCE: DECLES.001APC

CURRENT APPLICATION NUMBER: US/09/423,468A

CURRENT APPLICATION NUMBER: NL 1006000

PRIOR FILING DATE: 1997-05-07

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 7

LENGTH: 7

LENGTH: 7

LENGTH: 7

LENGTH: 7
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APPLICANT: AMGEN INC.

TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like

TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Center, Patent Operations/RRC
STREET: 1840 DeHavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: U.S.
ZIP: 91320-1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.7%; Score 24; DB 5; Length 7; 71.4%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.6%; Score 20; DB 4; Length 7; 50.0%; Pred. No. 3e+05; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENT NR-BERSE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04075
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Brassica oleracea
US-09-423-468A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 3, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
PCT-US95-04075-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 7 amino e
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FTLEISR 7
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2 TIELSK 7
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US-08-222-619-21
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Gaps

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2; Indels

unknown

STRANDEDNESS:

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OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Ribonucleotide reductase inhibitor peptide
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Patent No. 5574008
GENERAL INFORMATION:
APPLICANT: Johnson, William T.
APPLICANT: Yakubu-Madus, Fatima E.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
CORRESPONDENCES: 13
CORRESPONDENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.6%; Score 19; DB 3; Length 7; 60.0%; Pred. No. 3e+05; 1ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.5%; Score 18; DB 1; Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: residue 1: MOD_RES: ACETYLATION US-09-040-216-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 46285
ZIP: 46285
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,731
FILING DATE:
TITLE OF INVENTION: RIBONUCLECTIDE REDUCTASE; FILE REFERENCE: 9596-63U1; CURRENT APPLICATION NUMBER: US/09/040,216; CURRENT FILING DATE: 1998-03-17; EARLIER APPLICATION NUMBER: 08/919,748; EARLIER APPLICATION NUMBER: 60/025,146; EARLIER FILING DATE: 1997-08-28; NUMBER OF SEQ ID NOS: 61; SOFTWARE: Patentin Ver. 2.0; SOFTWARE: Patentin Ver. 2.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEB: Eli Lilly and Company/RSM STREET: Lilly Corporate Center CITY: Indianapolis STATE: IN COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maciak, Ronald S.
REGISTRATION NUMBER: 35,262
REFERENCE/DOCKET NUMBER: X963
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-1664
TELEPHAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 FTLEI 5
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1 FTLDL 5
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APPLICANT: Barry S. Cooperman, Harvey Rubin,
APPLICANT: Jerone Salem, and Alison L.; Fisher
TITLE OF INVENTION: Plasmodium falciparum Ribonu-
TITLE OF INVENTION: Cleotide Reductase, DNA Sequences Therefor and Peptide inhibit
TITLE OF INVENTION: Thereof"
NUMBER OF SEQUENCES: G.
CORRESSONDENCE ADDRESS;
ADDRESSES: The University of Pennsylvania
STREET: 3700 Market Street
GITY: Philadelphia
STREET: 3700 Market Street
GONGTUR: BM P62-3246
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 KD
COMPUTER: BM P62-3246
COMPUTER: US/A193
COMPUTER: US/A193
ATTORNEY/AGENT INFORMATION:
NAME: Worder-East 359-10
REFERENCE/DOCKET NUMBER: 395-10
TELECOMMUNICATION HUMBER: 395-10
TELECOMMUNICATION HU
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US-09-040-216-28
; Sequence 28, Application US/09040216
; Patent No. 6030942
; GENERAL INFORMATION:
; APPLICANT: COOPERMAN, ET AL., BARRY
; TITLE OF INVENTION: SMALL MOLECULES USFFUL FOR INHIBITING THE ACTIVITY OF
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                          2; Indels
                                                                                                                           Score 19; DB 5; Length 6; Pred. No. 3e+05; 2; Indels 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-136-743B-55; Application US/08136743B; Patent No. 5459063; GENERAL INFORMATION:
                                                                                                                      Query Match
Best Local Similarity 66,7%;
Matches 4; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
  ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04075-21
                                                                                                                                                                                                                                                    1 FTLEIS 6
                                                                                                                                                                                                                                                                                                           1 FTFEYS 6
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1 FTLDL 5
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    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    OTHER INFORMATION: Peptide
    US-09-657-332A-6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
PCT-US95-10793-4
; Sequence 4, Application PC/TUS9510793
; GENERAL INFORMATION:
; APPLICANT: Johnson, William T.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
; TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
; VORRESPONDENCE: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/RSM
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09876388

Patent No. 6593295

GENERAL INFORMATION:

APPLICANT: Bridon, Dominique P.

APPLICANT: Ezrin, Alan M.

APPLICANT: Leblanc, Benoit

APPLICANT: Leblanc, Anouk

APPLICANT: Leblanc, Anouk

APPLICANT: Leblanc, Anouk

APPLICANT: St. Pierre, Serge

TITLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES

FILE REFERENCE: 500862001610

CURRENT APPLICATION NUMBER: US/09/876,388

CURRENT PILING DATE: 2001-09-24
                                                                                                                                                                                             1; Indels
                                                                                                                                             Score 18; DB 4; Length 6;
Pred. No. 3e+05;
2; Mismatches 1; Indels
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Pred. No. 3e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-09-24

PRIOR APPLICATION NUMBER: 09/623,618

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: PCT/USOO/13563

PRIOR APPLICATION NUMBER: 60/159,783

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-05-17

NUMBER OF SEQ ID NOS: 35

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6
                                                                                                                                             Query Match 54.5%;
Best Local Similarity 50.0%;
Matches 3; Conservative ;
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50.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 3; Conserva
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1 FTSDVS 6
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1 FTSDVS 6
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US-09-876-388-6
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Patent No. 6514500

GENERAL INFORMATION:
APPLICANT: Bridon, Dominique P.
APPLICANT: Ezin, Alan M.
APPLICANT: L'Archeveque, Benoit
APPLICANT: Leblanc, Anouk
APPLICANT: Leblanc, Anouk
APPLICANT: St. Pierre, Serge
TITLE OF INVENTION: LONG LASTING SYNTHETIC GLUCAGON LIKE PEPTIDE (GLP-1)
FILE REFERENCE: 500862001600
CURRENT APPLICATION NUMBER: US/09/657,332A
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
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                           Gaps
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CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Synthetic
COTHER INFORMATION: Peptide
US-09-623-618B-6
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APPLICANT: Bridon, Dominique P.

APPLICANT: Ezin, Alan M.

APPLICANT: Ezin, Alan M.

APPLICANT: Ezin, Alan M.

APPLICANT: Esin, Alan M.

APPLICANT: Esin, Alan M.

APPLICANT: Esin, Alan M.

APPLICANT: Esin, Alan M.

APPLICANT: Leblanc, Anowh

APPLICANT: Esinge

TILLE OF INVENTION: LONG LASTING INSULINOTROPIC PEPTIDES

TILLE REFERENCE: 50086201620

CURRENT FILING DATE: 2000-09-05

PRIOR FILING DATE: 2000-05-17

PRIOR PPLICATION NUMBER: 60/159,783

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-10-15

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 6

TANDEL DETAILST
 Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 1; Indels
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Best Local Similarity 50.0
Matches 3; Conservative
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1 FTSDVS 6
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US-09-623-618B-6
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TOPOLOGY: linear
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2 FTSDVS 7
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2 FTSDVS 7
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APPLICANT: Johnson, William T.
APPLICANT: Yakubu-Madus, Fatima E.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE FRAGMENTS OF
TITLE OF INVENTION: GLUCAGON-LIKE INSULINOTROPIC PEPTIDE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company/RSM
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN
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ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,262
REFERENCE/DOCKET NUMBER: X9630
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-1664
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids

"TOTAL OF THE COMPANIENT OF THE COMPANIEN
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ZUR: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,731
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FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Maciak, Ronald S.
REGISTRATION NUMBER: 35,262
REFERENCE/DOCKET NUMBER: X963
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-1664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08297731 Patent No. 5574008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.0
Matches 3; Conservative
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide
PCT-US95-10793-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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1 FTSDVS 6
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; TYPE: PRT ; ORGANISM: Homo sapien US-09-218-363-23

Query Match 54.5%; Score 18; DB 4; Length 7; Best Local Similarity 75.0%; Pred. No. 3e+05; Matches 3; Conservative 1; Mismatches 0; Indels

0; Gaps

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1 FTLE 4 ||:| 2 FTME 5 ઠે

Db

Search completed: June 2, 2004, 19:01:06 Job time: 15.5 sec8

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

June 2, 2004, 18:54:42 ; Search time 13 Seconds (without alignments) 51.795 Million cell updates/sec Run on:

US-09-712-819D-13 31 1 LTLKLSR 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

457 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	ribosomal protein	cytochrome-c oxida	hypothetical prote	flagellar protein	cytotoxic T-lympho		phosphonoacetaldeh	glycoprotein compo	DNA topoisomerase	major fat-globule	hypothetical prote	hypothetical prote	6	Ig mu chain D regi	catch-relaxing pep	sex pheromone cCF1	myomodulin - Calif	pullulanase (EC 3.	copper resistance	T-cell receptor be				surface protein te	dnaA protein - Pse	1-1	MHC H2-L antigen -	T-cell receptor be	
SUMMARIES	ID	\$19630	T13892	T46627	E42364	I49424	JN0859	A28709	E48394	I48086	4	I40505	T14910	I48126	B33932	ECMUCR	A30812	A28340	PN0649	C41225	PT0525	PT0577	PT0565	PT0700	869237	B34835	A43766	I65546	PT0518	PT0662
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di	Query Match Length		35.5	.5	.5	.5	35.5	.5	5	5.	ιŲ	۳.	۳.	۳.	۳.	۳.	۳.	ب	Э.	0.	0.	Ō	0	0	0	0	0	0	0	0
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RESULT 1 S19630 ribosomal protein L30 - Streptomyces grise C; Species: Streptomyces griseus C;Date: 12-Feb-1993 #sequence_revision 12-C;Accession: S19630 R;Ochi, K. Int. J. Syst. Bacteriol. 42, 144-150, 1992 A;Title: Electrophoretic heterogeneity of A;Reference number: S19630; MUID:92144363; A;Accession: S19630 A;Molecule type: protein A;Residues: 1-7 <och> A;Residues: 1-7 <och> C;Superfamily: Escherichia coli ribosomal C;Superfamily: Escherichia coli ribosomal</och></och>	protein L30 Streptomyc -reb-1993 # n: S19630 st. Bacteric lectrophore e number: S: n: S19630 i type: prote rilly: Bscher: illy: Bscher:	in L3 1993 1993 9630 9630 sacter ophor ber: coch sourc Esche	ALI sin L30 - Streptomyces gr sptomyces griseus -1993 #sequence_revision 19630 sacteriol. 42, 144-150, 1 cophoretic heterogeneity aber: \$19630; MUID:921443 19630 s: protein 7 <0CH> Source: strain IFO 13189 Escherichia coli ribosom tein biosynthesis; ribos	Streptomyces griseus Tuence_revisic 42, 144-150, heterogeneit 130, MUID:9214 itrain IFO 131	otcom 144 1114 1010 1010 1011 1011 1011	Altreptomyces griaeus ence_revision 42, 144-150, heterogeneity 0; MUID:92144	ENTS us (fragment) Feb-1993 #text ribosomal prot PMID:1736962 protein L30	_change 06-Jun-1997 ein AT-L30 among actinomycete
Query Match Best Local Matches	cch al Sin 2;	Similarity 2; Conser	41. larity 40. Conservative	41.9% 40.0% ative	41.9%; 40.0%; ive	c	Score 13; DB 2; Length 7 Pred. No. 2.8e+05; Mismatches 0; Indel	7; ils 0; Gaps 0;

cytochrome-c oxidase (EC 1.9.3.1) chain I [imported] - river lamprey mitochondrion (f. Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Species: mitochondrion Lampetra fluviatilis (river lamprey)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: T13892
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Moll. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the A;Reference number: Z17775; MuID:97398704; PMID:9254918
A;Reference number: Z17775; MuID:97398704; PMID:9254918
A;Reference number: Jampa A;Reference DNA
A;Residues: Jampa A;Residues: Jampa A;Residues: Jampa Comparion C;Genetics:
A;Geneme: mitochondrion
A;Note: COI
C;Keywords: mitochondrion; oxidoreductase

Gaps .; 0 Query Match 35.5%; Score 11; DB 3; Length 3; Best Local Similarity 66.7%; Pred. No. 2.8e+05; Matches 2; Conservative 1; Mismatches 0; Indels

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peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JN0859
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A;Title: Isolation and characterization of angiotensin: JN0859
A;Molecule type: protein
A;Residues: 1-7 <MAT>
A;Experimental source: intestine
C;Comment: The carboxyl-terminus is essential for the protein's expression of angioten
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor
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C;Accession: A28709
R;Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
B;Ochemistry 27, 2229-2234, 1988
A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidencidue.
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R,Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-p II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
A;Accession: E48394
A;Status: preliminary
A;Molecule type: protein
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C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
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;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
     Gaps
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A;Accession: A28709
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <OLS>
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       Mismatches
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Best Local Similarity 66.7
Matches 2; Conservative
     2; Conservative
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                                                                                                                                    Appothetical protein c4 - loblolly pine
C; Species: Pinus taeda (loblolly pine)
C; Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C; Accession: T46627
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
R; Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
A; Reference number: Z23105
A; Reference number: Z23105
A; Accession: T46627
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-4 < CHA>
A; CTOSS-references: EMBL: U31309; NID: 9974285; PID: 9974292
A; Experimental source: strain s6PT2xs6FT3; 8 month seedlings
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E42364
flagellar protein flik - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 30-Sep-1993
C;Accession: B42364
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.
J. Bacteriol. 173, 3564-3572, 1991
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and seq A;Accession: E42364; MUID:91258342; PMID:1646201
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A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05745; NID:g497084; PIDN:AAB60481.1; PID:g642831
C;Keywords: hydrolase; serine proteinase
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66.7%; Pred. No. 2.8e+05;
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Best Local Similarity 66.7
Matches 2; Conservative
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A;Molecule type: DNA
A;Residues: 1-5 <VOG>
A;Cross-references: GB:M62408
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the genome of Chinese hamste
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C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14910
R;Kircher, S.; Ledger, S.; Hayashi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis
A;Accession: T14910
A;Accession: T14910
A;Accession: T14910
A;Accession: Lype: mRNA
A;Residues: 1-5 <KIR>
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10810; NID:g3336904; PIDN:CAA71769.1; PID:g3336905
A;Experimental source: ssp. Hamburger Schnitt
Eur. J. Biochem. 158, 505-510, 1986
A;Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA A;Reference number: 140503; MUID:86274732; PMID:3525162
A;Recession: 140505
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C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I48126
R;Elliott, E.M.; Sarangi, F.; Henderson, G.; Ling, V.
Can. J. Biochem. Cell Biol. 63, 511-518, 1985
A;Title: Cloning of 11 alpha-tubulin gene sequences from the genome of Chines A;Reference number: 148126; MUID:86001952; PMID:2931165
A;Accession: I48126
A;Accession: I4826
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M25895; NID:g341417; PIDN:AAA74493.1; PID:g516601
C;Genetics:
A;Introns: 3/3
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C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-4 <RES>
A, Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1;
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Pred. No. 2.8e+05;
1; Mismatches 0; Indele
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2 VSR 4
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iochem. Mol. Biol. Int. 29, 545-554, 1993
Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
I-like sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: 148086
R;Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.
J. Biol. Chem. 270, 25850-25858, 1995
A;Title: Molecular cloning and characterization of the promoter for the Chinese hamster A;Reference number: 148086; MUID:96029684; PMID:7592770
A;Accession: 148086
A;Accession: 148086
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <RES>
A;Cross-references: EMBL:U34196; NID:g1041231; PIDN:AAC52315.1; PID:g1041232
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C;Species: Bacillus stearothermophilus
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40505
R;Waye, M.M.; Winter, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       major fat-globule membrane protein GP 55 - guinea pig (fragment)
C,Species: Cavia porcellus (guinea pig)
C,Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA topoisomerase II alpha - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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A, Residues: 1-7 <MAT>
A, Experimental source: milk
A, Note: sequence extracted from NCBI backbone (NCBIP:131450)
C, Keywords: glycoprotein
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Matches 2; Conservative
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 < MAT>
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4 ELAR 7
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Ig mu chain D region (D23) - mouse
C; Species: Mus musculus (house mouse)
C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 16-Aug-1996
C; Accession: B33932
R; Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
R; Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A; Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1 A; Reference number: A33932; MUID:89282823; PMID:2499887
A; Accession: B33932
A; Atatus: preliminary
A; Molecule type: mRNA
A; Residues: 1-6 cBAC>
A; Cross-references: GB:M27107
C; Keywords: immunoglobulin
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A; Molecule type: protein
A; Residues: 1-7 < HIR>
C; Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxat C; Superfamily: unassigned animal peptides
C; Superfamily: unassigned animal peptides
C; Keywords: amidated carboxyl end; hormone; retractor muscle
E; 7/Modified site: amidated carboxyl end (Leu) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catch-relaxing peptide - blue mussel
N;Alternate names: CARP
C;Species: Mytilus edulis (blue mussel)
C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C;Accession: A29342
R;Hirata, T.; Kubota, I.; Takabatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.
Brain Res. 422, 374-376, 1987
A;Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.
A;Reference number: A29342; MUID:88052022; PMID:3676797
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5 LRL 7
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OM protein - protein search, using sw model

June 2, 2004, 18:47:58; Search time 10 Seconds (without alignments) 36.449 Million cell updates/sec Run on:

US-09-712-819D-13 31 1 LTLKLSR 7 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

88 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	P10420 mytilus edu		P16101 alcaligenes	P80630 zea mays (m	P82100 litoria rub	P42564 hirudo medi	P99025 mus musculu	P24272 vibrio fisc	P13071 citrobacter	σ	P25154 oryctolagus		P23210 herpes simp		achat	P35920 achatina fu	P35921 achatina fu	P42562 hirudo medi		P58707 anthopleura					P38499 procambarus		P38498 procambarus	P56576 rattus norv	P01157 homo sapien	P19918 pseudomonas	m	5	P01162 macrocallis
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CCF1 ENTFA STANDARD; PRT; 7 AA.

P20104;
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
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Sex pheromone CCF10.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus faecalis).

RESULT 2
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anthopleura homo sapien bothrops in artioposthi periplanero daucus caro litoria rub litoria rub escherichia lactobacill moniezia ex		ර් ද	namoto N., inglia."; (contraction)		Gaps	
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មា	T 1 MYTED CARP MYTED	P10420; 01-MAR-1989 (Rel. 10, Created) 01-MAR-1989 (Rel. 10, Last sec 01-MAR-1989 (Rel. 10, Last and Catch-relaxing peptide (CARP). Mytilus edulis (Blue mussel). Mytiloidea; Metazoa; Mollusca; Mytiloidea; Mytilidae; Mytilus NCBI_TaxID=6550;		A293 A293 One; RES ENCE	fatch scal Similarity s 2; Conser	3 LK - 5 LR
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Neuropeptide, Amidation.
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Pernollet J.-C., Zivy M., de Vienne D.;
"The maize two dimensional gel protein database: towards an integrated genome analysis program.";
Theor. Appl. Genet. 93:997-1005(1996).
-!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 6.0, its MW is: 30.0 kDa.
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J. Biochem. 88:197-203(1980).
-!- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2)
PIR; A15398; A15398.
Oxidoreductase.
-!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PCF10.
PIR, A30812, A30812.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDLINE=81006769; PubMed=6997283;
Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
"Identification and properties of the prosthetic group of choline
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01-OCT-1996 (Rel. 34, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
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CHOX ALCSP

ID CHOX ALCSP

AC P16101;

DT 01-APR-1990 (Rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last annotation update)

DT 01-APR-1990 (Rel. 14, Last annotation update)

DF 01-APR-1990 (Rel. 13.17) (Fragment).

OS Alcaligenes Sp.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                        32.3%; Score 10; DB 1; Length 7; llarity 66.7%; Pred. No. 1.4e+05; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 7;
                                                                                      7 AA; 790 MW; 72C9D2C731B2C740 CRC64;
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100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alcaligenaceae; Alcaligenes.
NCBI_TaxID=512;
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Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conserv
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Zea mays (Maize)
                                                                                                                                                                                                        1 LTL 3
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2 VTL 4
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UC24 MAIZE
ID UC24 MAIZE
AC P80630;
DT 01-OCT-1996 ()
DT 01-OCT-1996 ()
                                                                  Pheromone.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=92195954; PubMed=1686933;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae,
Pelodryadinae, Litoria.
NCBI_TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAES HIRME STANDARD; PRT; 7 AA.
P42564;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFamide-like neuropeptide GGKYMRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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                                                                                                               1; Indels
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                                                      29.0%; Score 9; DB 1; Length 7; larity 66.7%; Pred. No. 1.4e+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 25.8%; Score 8; DB 1; Length 5; Similarity 33.3%; Pred. No. 1.4e+05; 1; Conservative 2; Mismatches 0; Indelt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
MOD RES 5 AMIDATION.
SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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AMIDATION

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SEQUENCE FROM N.A.
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SEQUENCE
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Matches
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01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site for the lux operon.";

J. Bacteriol. 172:6797-6802(1990).

-!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.

IT IS A COMPONENT OF THE FAITY ACID REDUCTASE COMPLEX RESPONSIBLE
FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP cyclohydrolase I. This inhibition is reversed by L-phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91072226; PubMed=2254256;
Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GCHFR OR GFRP.
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NCBI_TaxID=668;
                                                                                                                                                                                                                                                                                            Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X., Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                    Query Match 25.8%; Score 8; DB 1; Length 7; Best Local Similarity 50.0%; Pred. No. 1.4e+05; Matches 2; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; DB 1; Length 7;
Pred. No. 1.4e+05;
1; Mismatches 1; Indela
 858 MW; 69D4068B53387810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               7 AA; 806 MW; 71B5B057273B4700 CRC64;
                                                                                                                                        7 AA.
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                                                                                                                                                                                                                                                                                                                                                            (By similarity).
-!- SUBUNIT: Homodimer (By similarity)
                                                                                                                                                                                                                                                                                                                   Cowthorne M.;
Submitted (AUG-1998) to Swiss-Prot.
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Similarity 50.0%;
2; Conservative 1
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                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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7 AA;
                                                                                                                                                                                                                                                TaxID=10090;
                                                               4 KLSR 7
                                                                                    3 KYMR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LKLS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LLIS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio fischeri.
                                                                                                                                                                                                                                                                       SEQUENCE.
TISSUE=Liver;
                                                                                                                                         MOUSE
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SEQUENCE
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LUXE_VIBFI
ID _LUXE_V
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
-!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(RC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Citrobacter freundii.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 22.6%; Score 7; DB 1; Length 3; Local Similarity 50.0%; Pred. No. 1.4e+05; leb 1; Conservative 1; Mismatches 0; Indels
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PIR; 140697; 140697.

InterPro; IPR005814; Aminotrans 3.

PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.

Biotin biosynthesis; Transferase; Aminotransferase;

Pyridoxal phosphate.

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Luminescence; Ligase.
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Flengsrud R., Skjeldal L.;
"Two-dimensional gel electrophoresis separation and N-terminal sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806(1998).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Unknown protein CP 6 from 2D-page (Fragment).
Clostridium pasteurianum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiam.
Clostridium.
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VP19_HSV1K
ID VP19_HSV1K
STANDARD; PRT; 6 AA.

AC P232I0;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.6%; Score 7; DB 1; Length 6; 25.0%; Pred. No. 1.4e+05; vative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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MEDLINE=91101287; PubMed=1846198;
Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
NCBI_TaXID=10306;
                                                                                                                                                                                                                                          NON-TER 6 6 8 SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 6 AA; 657 MW; 605B1DC1A45A8000 CRC64;
                                                       S9C.
-!- SUBUNIT: Homotetramer.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to peptidase family
PIR; A49792; A49792.
MEROPS; S09.004; -.
                                                                                                                          InterPro; IPR002471; Pept S9 AS.
PROSITE; PS00708; PRO ENDOPEP SER; PARTIAL.
Hydrolase; Acetylation.
MOD_RES 1 1 ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
STRAIN=W5;
MEDLINE=98291870; PubMed=9629918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.0 Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::
3 TAEI 6
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Matches
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MEDLINE=9222120; PubMed=1807161;

Krishna R.G., Chin C.C.Q., Wold F.;

"N-terminal sequence analysis of N alpha-acetylated proteins after unblocking with N-acylaminoacyl-peptide hydrolase.";

Anal. Biochem. 199:45-50(1991).

-!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
-!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)0 = acylamino acid
                                                                                                             Gaps
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MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
Electrophoresis 15:735-745(1994).
Protein is: 6.6, its MW is: 19 kDa.

NON TER
SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (Aragment).
                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
111-1-11-12-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                             0; Indels
                                                     Length 5;
  5 AA; 582 MW; GAAABIBIA6F00000 CRC64;
                                                   11 22.6%; Score 7; DB 1; Li illarity 50.0%; Pred. No. 1.4e+05; Conservative 1; Mismatches 0
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Matches 1; Conserv
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UF01_MOUSE

AC P38639;
DT 01-OCT-1994
DT 01-OCT-1994
DT 15-MAR-2004
DE UNKNOWN Prot
OC MAMMALIA; EU
OC HISSUE=FIDEC
RA MEDLINE=950C

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P25154;
    SQ SEQUENCE
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Silverstein S., Wagner E.K.;
"Analysis of the herbes simplex virus type 1 promoter controlling the expression of UL38, a true late gene involved in capsid assembly.";
J. Virol. 65:769-786(1991).
-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
-!- SIMILARITY: Belongs to the herpesviruses VP19C family.
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TISSUE=Larva;

MEDLINE=98054539; PubMed=9392829;

Buve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

-! SIMILARITY: Belongs to the allatostatin family.

Neuropeptide; Amidation.

MOD_RES
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M57646; AAA45830.1; -.. Capsid assembly; Coat protein; DNA-binding.
NON TER 6 6
SEQUENCE 6 AA; 703 MW; 67376451A335F000 CRC64;
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7 AA; 873 MW; 672879CABB569350 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 7.
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(Rel. 29, Last sequence update)
(Rel. 30, Last annotation update)
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P35919;
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ID _ALL7_CYDPO
AC P82158;
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Achatina fulica (Giant African snail).
Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Sigmurethra, Achatinoidea, Achatinidae, Achatina.
NCBI_TaxID=6530,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                       TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
Minakata H., Ikeda T., muneoka Y., Kobayashi M., Nomoto K.;
"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica.";
ganglia of the African giant snail, Achatina fulica.";
ganglia of the African giant snail, Achatina fulica.";
-1- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.
PIR; $33245; $33245.
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7 AA, 993 MW; 7362D5B69B041310 CRC64;
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Job time : 11 secs
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Q66205 transmissib P70804 azotobacter O34028 sphingomona Q9c5b3 arabidopsis Q9yve3 human adeno Q6f13 cherry leaf Q9yir0 human adeno Q6f19 human adeno Q9yir0 human adeno Q42564 fugu rubrip P83073 bacillus ce Q47029 enterobacte P72081 nocardia la Q54248 streptomyce Q28742 oryctolagus P92214 amblyopyrum P92214 amblyopyrum P92210 amblyopyrum P92210 peridictyon P92210 bromus iner P92210 bromus iner P92210 agropyron c P92387 henrardia p P92210 thinopyrum P92210 agropyron c P92240 thinopyrum P92210 australopyr P92230 heteranthel

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STRAIN=D273-10B;
MEDLINE=81069885; PubMed=6254986;
Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
"Assembly of the mitochondrial membrane system: Structure and nucleotide sequence of the gene coding for subunit 1 of yeast cytochrome oxidase.";
J. Biol. Chem. 255:11927-11941(1980).
EMBL; V00694; CAA24066.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Q66205
Q34028
Q34028
Q9C5B3
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Q9
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P92440
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Matches 3
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295945
ID 0959-DT 001-F
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                                                                                                                                                                                     June 2, 2004, 18:48:29 ; Search time 34.5 Seconds (without alignments) 64.018 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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P82182
Q8GL00
Q8JE81
P82541
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P83308
O07354
Q8GL12
Q8GL04
Q15897
Q7Z1C0
P93233
Q8K3H6
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mc:*
sp_organelle:*
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sp_rvirus:*
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sp_rodent:*
sp_virus:*
sp_vertebrate:*
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31
1 LTLKLSR 7
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Match Length
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Perfect score:
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No.
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Gaps

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Ribosomal protein; Chloroplast; rRNA-binding.
NON TER 6 6
SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
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Best Local Similarity
Matches 2; Conserv
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Q8GL00
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XA MEDLINE=20435798; PubMed=10874046;

RA Yamaguchi K., Subramanian A.R.;

RT "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

RL "The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

RL "Eiol. Chem. 275:28466-28482 (2000).";

CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

CC -!- FUNCTION: THIS PROTEIN ALL PLANT TISSUES.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.

CC -!- SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.

CC -!- SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.

CO; GO:00095735; F:rrna binding; IEA.

DR GO; GO:0003735; F:structural constituent of ribosome; IEA.

DR InterPro; IPR002363; Ribosomal LIOeub.

DR RIBOSOMAL LIO; PARTIAL.

KW Ribosomal protein; Chloroplast; rRNA-binding.
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X MEDLINE=20435798; PubMed=10874046;

X Yamaguchi K., Subramanian A.R.;

Yamaguchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the 50 ·S subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 275:28466-28482(2000).

J. Biol. Chem. 275:28466-28482(2000).

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.

C. !- FUNCTILON: THIS PROTEINS.

C. !- FUNCTILON: THIS PROTEINS.

C. !- SIMILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOMAL PROTEINS.

GO; GO:0009507; C:chloroplast; IEA.

R GO; GO:0009735; F:structural constituent of ribosome; IEA.

R GO; GO:0003735; F:structural constituent of ribosome; IEA.

R RDOSITE; PS01109; RIBOSOMAL_LIO; PARTIAL.
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P82181
P82181;
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach) Streptophyta; Eukaryota, Viridiplantae, Streptophyta; Eukaryota, Viridiplantae, Streptophyta; Eukaryota, Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P82182;
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AA; 675 MW; 6321B415B05DB000 CRC64;
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Best Local Similarity 66./
Lac 2; Conservative
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SEQUENCE FROM N.A.
STRAIN=CA15;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142106; AAN17857.1; -
GO; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid.
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MEDLINE=22056123; PubMed=12060770;
Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
Hoffmann D., Korn K., Selbig J.;
"Diversity and complexity of HIV-1 drug resistance: A bioinformatics approach to predicting phenotype from genotype.";
Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
EMBL; AF347267; AAK32344.1; -.
NON TER 1 1
SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-13.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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h 35.5%; Score 11; DB 10; Length 6; Similarity 66.7%; Pred. No. 1e+06; 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.5%; Score 11; DB 2; Length 7; 66.7%; Pred. No. 1e+06; 1; Mismatches 0; Indels trive
                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PF-50 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Truncated pol protein (Fragment).
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Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCBI_TaxID=11676,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER 1 1 1
SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;
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Best Local Similarity 66.7
Matches 2; Conservative
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Gaps

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P82541

RESULT 6 P82541

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
PubMed=6137771;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
                                                                                                                                                                                                                      Proteomics 2:765-774 (2002).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN PROTEIN IS: 15 KDA.
NON_TER 1 1
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MEDLINE=91282758; PubMed=1840486;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
Sato H., Aono S., Kashiwamata S., Koiwai O.;
"Genetic defect of bilirubin UDP-glucuronosyltransferase in the
"Properbilirubinemic Gunn rat.";
Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
EMBL; S38636; AAB19259.1; -.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                       Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.; "High pressure effects step-wise altered protein expression in Lactobacillus sanfranciscensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 2; Length 7; Pred. No. 1e+06; 0; Indels 1; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
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P83308;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
FMRFamide-like neuropeptide (LPLRF-amide).
Gallus gallus (Chicken).
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SEQUENCE 4 AA; 473 MW; 633732C42000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.3%;
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                                                  PubMed=12112860;
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1 VTL 3
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SEQUENCE
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Q08433;
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Matches
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Q08433
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                                                  STREETERS
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SEQUENCE, ALWARO, TISSUE=Leaf;

STRAIN=cv. ALWARO, TISSUE=Leaf;

RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;

RT The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";

The plastid ribosomal proteins. Identification of all the proteins in the small subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 37:28455-28465(2000).

CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

CC -!- FUNCTILLAR LOCATION: CHLOROPLAST.

CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.

CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.

CC -!- MASS SPECTROMETRY: MW=10495; METHOD=ELECTROSPRAY.

CC -!- MASS SPECTROMETRY: MP=10477.0; ME
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unknown protein from 2D-page (Fragment).
Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes, Lactobacillales; Lactobacillus.
                                           Score 11; DB 15; Length 7; Pred. No. 1e+06; 0; Indele 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.3%; Score 10; DB 10; Length 6; 66.7%; Pred. No. 1e+06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 30S ribosomal protein S19 beta (Fragment).
Spinacia oleracea (Spinach).
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                                        35.5%;
llarity 66.7%;
Conservative 1
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Query Match
Best Local Similarity
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Matches 2; Conserv
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STRAIN=DSM 20451;
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3 ITL 5
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SEQUENCE FROM N.A.
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SEQUENCE
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Q15897;
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Q8GL04
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MEDLINE=99231861; PubMed=10217509;
Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
"Organization and expression of nitrogen-fixation genes in the aerobic nitrogen-fixing unicellular cyanobacterium Synechococcus sp. strain RF-1.";
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STRAIN=N40;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechococcus sp. (strain PCC 8801 / RF-1) (Cyanothece PCC 8801).
Bacteria; Cyanobacteria; Chroococcales; Cyanothece.
NCBI_TaxID=41431;
"A novel active pentapeptide from chicken brain identified by antibodies to FMRPamide.";
Nature 305:328-330(1983).
-!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.

GO: GO: 0007218; P: neuropeptide signaling pathway; TAS.
Neuropeptide; Amidation.

MOD RES 5 AA; 645 MW; 69D4073767400000 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON TER 1 1 1
SEQUENCE 7 AA; 849 MW; 7412C72AA9D5B030 CRC64;
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EMBL; AF003700; AAC35193.1; -..
NON TER 1
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007354;
01-JUL-1997 (TrEMBLrel. 04,
01-JUL-1997 (TrEMBLrel. 04,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 28.6
Matches 2; Conservative
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Les 2; Conserv
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1 ISFDLVR
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Q8GL12;
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007354
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Matches
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STRAIN=93-0107;
Stevenson B., Miller J.C.;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142103; AAN17848.1; -.
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                        Gaps
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TISSUE=Placenta;

Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,

Caskey C.T.H.;

"Isolation of chromosome-specific genes by reciprocal probing of

arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL; L32077; AAA73887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Borrelia burgdorferi (Lyme disease spirochete).
Plasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY142100; AAN17911.1; -. GO:0046821; C:extrachromosomal DNA; IEA. Plasmid.
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                                                                                                                                                                                                                            Length 7;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                   1 1 7 AA; 849 MW; 6337244330569ED0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                               Gaps
                                                                                                                                                                                                                                                                                        Caranthabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                  Query Match 29.0%; Score 9; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
(Fragment).
LE-ACSIB.
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STRAIN=Bristol N2;
Bradshaw H., Graves T., Blair T.;
"The sequence of C. elegans cosmid W01B11.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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1e+06;
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Last annotation update)
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Hypothetical protein.
SEQUENCE 7 AA; 874 MW; 72D1A9DB5041A6F0 CRC64;
                           7 AA; 814 MW; 672B1DD3372046B0 CRC64;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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01-OCT-2003 (TrEMBLrel. 25, Las
01-OCT-2003 (TrEMBLrel. 25, Las
Hypothetical protein W01B11.6.
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Best Local Similarity 33.3%;
Matches 1; Conservative
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P93233
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OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; endicotyledons; core endicots; asterids; OC lamidds; Solanales; Solaname.

OX NCBI_TAXID=4081;
RN MCBI_TAXID=4081;
RN MEDLINE=97351561; PubMed=9207843;
RA PEQUENCE FROM N.A.
RY MEDLINE=97351561; PubMed=9207843;
RA Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT Synthase genes by elicitor in suspension cultures of tomato
RT Grooperation esculentum).";
RT Clycoperation of seven 1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
OG: GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
OG: GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
OG: SEQÜENCE 7 AA; 828 MW; 718412C7377415D0 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CO: Clob time : 35.5 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model OM protein - protein search, using 2, 2004, 18:47:08; Search time 49 Seconds (without alignments) 40.364 Million cell updates/sec June Run on:

BLÓSUM62 Gapop 10.0 , Gapext 0.5 US-09-712-819D-13 31 1 LTLKLSR 7 Title: Perfect score: Scoring table: Sequence:

1586107 seqs, 282547505 residues Searched:

hits satisfying chosen parameters: Total number of

92273

Minimum DB seq length: 0 Maximum DB seq length: 7

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_29Jan04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

uo.	Human RSV	Respirato	SYNAGIS a	Haemagglu	Rheumatoi	Rheumatoi	Vascular	Vascular	Vascular	DPI trypt	Schizophr	Depressio	Schizophr	Human API	Human RSV	Multiple	Multiple	Prostate	Respirato	Breast ca	Alzheimer	SYNAGIS a	S. cerevi	Cauliflow	Nucleotid
Description	Abp66518	Abu69381	Ade35876	Aaw69269	Aay42013	Aay41889	Abb55870	Abb56283	Abb55981	Aau28602	Aau24969	Aau26249	Aau15313	Abb52355	Abp66489	Abg78901	Abg78730	Abp58010	Abu69352	Abp57255	Abr 59042	Ade35847	Aae21359	Aaw82668	Aab02931
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QI	ABP66518	ABU69381	ADE35876	AAW69269	AAY42013	AAY41889	ABB55870	ABB56283	ABB55981	AAU28602	AAU24969	AAU26249	AAU15313	ABB52355	ABP66489	ABG78901	ABG78730	ABP58010	ABU69352	ABP57255	ABR59042	ADE35847	AAE21359	AAW82668	AAB02931
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% Query Match Length	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	φ	7	7
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Score	20	20	20	19	19	19	. 61	19	19	19	19	19	19	19	19	19	6 H	49	19	19	19	19	18	18	18
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4 AAE10492 5 ABP66389	5 ABP66485 5 ABP66485 5 ABP49796	5 ABP48455 5 ABP51172 5 ABP49577	5 ABP49790 5 ABB07139	5 AAE28044 6 ABU69348	6 ABU69252 6 ABU69313	7 ADA65532 7 ADA62425	7 ADA64000 7 ADA65571	7 ADA65573 7 ADE35808
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ALIGNMENTS

Human RSV antibody VL CDR2 fragment ABP66518 standard; peptide; 7 AA. 04-DEC-2002 ABP66518;

Human, variable heavy domain; variable light domain; CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.

Homo sapiens

WO200243660-A2.

06-JUN-2002

28-NOV-2001; 2001WO-US044807

28-NOV-2000; 2000US-00724396 28-NOV-2000; 2000US-00724531

(MEDI -) MEDIUMMUNE INC.

Johnson LS; Young JF, Koenig S,

WPI; 2002-706803/76.

Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically binds to RSV antigen.

Claim 8; Page 55; 298pp; English.

The invention relates to a novel antibody comprising a variable heavy (VH) domain, variable light (VL) domain, VH complementarity determining region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the antibody immunospecifically binds to a respiratory syncytial virus (RSV) antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV, and immunostimulant activity. The polynucleotides of the invention may

Query Match

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have a use in a vaccine, and in gene therapy. The antibody is useful for treating or ameliorating a RSV infection in a human. The antibody is also useful for preventing, treating or ameliorating one or more symptoms associated with RSV infection in a mammal, e.g. cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency or acquired immunodeficiency, or after a bone marrow transplant. The sequence represents a complementary determining region peptide from a human RSV antibody of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Respiratory syncytial virus; RSV; vaccine; antibody; variable heavy domain; VH; variable light domain; VH; complementarity determining region; CDR; CDR1; CDR2; CDR3; RSV infection; cystic fibrosis; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immune deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, useful for preventing or treating a respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an antibody comprising a variable heavy (VH) or variable light (VL) domain or complementarity determining region (CDR), such as CDR1, CDR2, or CDR3, which immunospecifically binds to a respiratory syncytial virus (RSV) antigen and is not SYNAGIS (RTM). The antibody, pharmaceutical compositions and methods are useful for preventing, treating or ameliorating a RSV infection in patients with cystic fibrosis, bronchopulmonary dysplasia, congenital heart disease, congenital immunodeficiency, or acquired immune deficiency, or patients having had a bone marrow transplant or the elderly. This is the amino acid sequence of a respiratory syncytial virus (RSV) antibody peptide
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Respiratory syncytial virus (RSV) antibody fragment #126.
                                                                                                                                                                                                            Score 20; DB 5; Length 7; Pred. No. 1.4e+06; 1; Mismatches 0; Indels
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                                                                                                                                                                                                            h 64.5%;
Similarity 80.0%;
4; Conservative
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ABU69381
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Sequence 7 AA;

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The invention relates to a method of preventing, treating or ameliorating on one or more symptoms associated with a respiratory syncytial virus (RSV) infection in a mammal. A sustained release formulation comprising one or more antibodies or their fragments that immunospecifically bind to one or more RSV antigens and a pharmaceutical composition comprising one or more artibodies or their fragments that immunospecifically bind to one or more RSV antigens formulated for pulmonary delivery is useful for preventing, treating or ameliorating one or more symptoms associated with a RSV infection in a mammal by administering the formulation to the mammal, or the composition to the lungs of the mammal. The antibodies bind to RSV antigen with a high affinity and/or high avidity. The methods use lower doses of antibodies which immunospecifically bind to RSV antigen, and which provide a more effective prophylaxis. The present sequence region based on the SYNAGIS antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preventing, treating or ameliorating symptoms associated with respiratory syncytial virus infection in mammal by administering antibodies or their fragments that immunospecifically bind to RSV antigens.
                                                                                                                                                                                                                                                                                                              respiratory syncytial virus; RSV infection; high affinity antibody; high avidity antibody; low antibody dose; more effective prophylaxis; complementarity determining region; CDR; human.
                                  Gaps
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64.5%; Score 20; DB 6; Length 7; llarity 80.0%; Pred. No. 1.4e+06; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                   ADE35876 standard; peptide; 7 AA.
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80.0%;
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(KOEN/) KOENIG S.
(JOHN/) JOHNSON L S.
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AAY42013 standard, peptide, 7 AA.

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This sequence represents a fragment of the heavy chain (HAI) of the heamagglutinin of influenza virus. This sequence was used to test the acryloylated peptide polymer of the invention. The peptide polymers are used to raise an immune response to a peptide epitope (such as this sequence), and also as diagnostic tools. Polymers (molecular wt. >600 kDa.) can be prepared with virtually any number of the same or different epitopes by a method that allows purification of the individual determinants, avoids errors inherent in long sequential syntheses in which protected peptide fragments are not used, thus avoiding solubility and purification problems. Multiple copies of many different peptide can do purification of the range of T cell epitopes required for outbred pathogenic serodemes, thus making them a significant advance in synthetic vaccine technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acryloylated peptide polymers - useful for synthetic vaccine technology, for raising an immune response to peptide epitope and as diagnostic tool
                                                                                                                                       Acryloylated peptide polymer; immune response; peptide epitope; synthetic vaccine; enzymatically cleavable site.
                                                                                                                                                                                                                                                  /note= "linked to acryloylated peptide polymer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jackson DC, Obrien-Simpson NM, Brown LE, Zeng W, Brandt ER, Good MF;
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNCIL QUEENSLAND INST MEDICAL RES. COMMONWEALTH SCI & IND RES ORG. UNIV MELBOURNE. HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                         Haemagglutinin heavy chain (HA1) fragment
                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3xample 1; Page 20; 77pp; English.
             AAW69269 standard; peptide; 7 AA.
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                                                                           29-OCT-1998 (first entry)
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                                                                                                                                                                                                                                    disc-difference
                                                                                                                                                                                       Influenza virus.
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03-OCT-1997;
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                                                                                                                                                                                                                                                                                                                  L3-AUG-1998
                                             AAW69269;
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AAW69269
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arthritis (RA) using two-dimensional electrons or numerate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an analysing a sample of serum or plasma and optionally comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen (feature whose relative abundance correlates with the presence or absence of RA, and (c) comparing the abundance of each chosen feature in the cample with the abundance of that chosen feature in serum or plasma from or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-c diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as C protocols. AAY41844 to AAY42100 represent RPI peptides, AAY42101 to AAY42103 represent expression reference protein isoform peptides and AAZ5066 to AAZ25068 represent expression function of antibodies or seed in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A method has been developed for the diagnosis of human rheumatoid
                                                                                                                                                  Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
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                                                                                                              Rheumatoid arthritis diagnostic protein isoform peptide #164.
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                                                                          (first entry)
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                                                                           09-DEC-1999
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Score 19; DB 2; Length 7; Pred. No. 1.4e+06; 1; Mismatches 0; Indels

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ABB55870;

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Human, rheumatoid arthritis, RA, diagnosis, RPI, RADF, detection, rheumatoid arthritis diagnostic feature, ERPI, synovial fluid; rheumatoid arthritis diagnostic protein isoform, screening, expression reference protein isoform, prognosis.
                                               Rheumatoid arthritis diagnostic protein isoform peptide #40.
                                                                                                                                                                                                                                     Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                     OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                             Disclosure; Page 18; 157pp; English.
AAY41889 standard; peptide; 7 AA
                                                                                                                                                                      98GB-00005477.
                                                                                                                                                     99WO-GB000763.
                               (first entry)
                                                                                                                                                                                                     Parekh RB, Patel TP,
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                                                                                                                                                                                                                                              electrophoresis.
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                               09-DEC-1999
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Townsend RR

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dimensional array of features. The method can be used for screening, dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the cample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-catagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic activity and in soforms (RPIS), and for production of antibodies to protocols. AAY41844 to AAY42100 reference protein isoform peptides and AAY42103 represent expression reference protein isoform peptides and AAY42103 represent expression reference protein isoform peptides and AAX25066 to AAX25068 represent degenerate probes for RPIS, which are all used in the exemplification of the present invention
A method has been developed for the diagnosis of human rheumatoid
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61.3%; Score 19; DB 2; Length 7;
66.7%; Pred. No. 1.4e+06;
ive 1; Mismatches 1; Indels
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ABB55870 standard; peptide; 7 AA.
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening, diagnosis or prognosis of vascular dementia (VD), useful for determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
                                                                                                     Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
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66.7%; Pred. No. 1.4e+06;
iive 1; Mismatches 1; Indels
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                                                                   Vascular dementia-associated protein isoform (VPI) 70.
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                                                                                                                         diagnosis; prognosis; gene therapy
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                                                                                                                                                                                                                                                                 14-MAR-2001; 2001WO-GB001106.
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28-NOV-2000; 2000US-00724391.
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                                                                                                                                                           Homo sapiens.
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                                 15-FEB-2002
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The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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                                                                                                                                                                                                  Screening, diagnosis or prognosis of vascular dementia (VD), useful determining stage of VD and monitoring the effect of VD therapy, comprises analyzing body fluid by 2-dimensional electrophoresis for features correlated with VD.
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                                                                 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                                             Parekh RB, Rohlff C;
                                                                                                                                                                                                                                                                                                                     Claim 6; Page 33; 151pp; English.
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
24-NOV-2000; 2000GB-00028734
28-NOV-2000; 2000US-00724391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to screening, diagnosis or prognosis of Vascular Dementia (VD) in a subject comprising analysing body fluid from the subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of features containing at least one chosen feature whose relative abundance correlates with the presence, absence, stage or severity of VD or predicts the onset or course of VD, especially detecting in a sample of cerebrospinal fluid (CSF) from the subject one of 223 VD-associated protein isoforms (VPIS) (ABB55801-ABB56295) as fully defined in the specification. Detecting VD-associated features and VPI is useful for the screening, diagnosis or prognosis of VD, for determining the stage or severity of VD, for identifying a subject at risk of VD or for monitoring the effect of therapy administered to a subject having VD. Nucleic acids encoding a VPI or inhibiting the function of a VPI are useful for the treatment of VD and for gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 40; 151pp; English.
                                                                                                                                                                               15-MAR-2000; 2000GB-00006285.
24-NOV-2000; 2000GB-00028734.
28-NOV-2000; 2000US-00724391.
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TFELSR
                                             WO200169261-A2.
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   Homo sapiens.
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Best Loc Matches

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RESULT 9 ABB55981

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Gaps

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Tyson KL;

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                                                                                                                                The present invention relates to the identification of depression associated protein isoforms (DPIs), particularly the tryptic digest peptides of these proteins. Some of the DPIs (AAU28404-AAU28625) described are decreased in the cerebrospinal fluid (CSF) of BAD (bipolar affective disorder) subjects, whilst other DPIs (AAU28626-AAU28887) are increased in BAD subjects. Also described are peptide sequences identified from DPI-45 and DPI-213 and the nucleic acid sequence they are encoded by. The sequences of the invention are useful for clinical screening, diagnosis, prognosis, therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also known as bipolar mood disorder, BP), maniac-depressive illnesses, attention deficit disorders. The present sequence represents one of the DPI tryptic digest peptides of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New schizophrenia associated protein isoforms and encoding nucleic acid molecules, useful for treatment, diagnosis and prognosis of schizophrenia and screening for potential drugs for treatment and new drug targets.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizophrenia-associated protein isoform; SPI, SPI-206; SPI-238; SPI-240; neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.
                               Novel nucleic acid encoding a protein associated with bipolar affective disorder, which is used for diagnosis, prophylaxis and therapy of neuropsychiatric disorders, such as bipolar affective disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rohlff C, Terrett JA, Tyson KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 19; DB 4; Length 7; Pred. No. 1.4e+06; i Mismatches 1; Indels
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                                                                                                    Disclosure; Page 34; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU24969 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   61.3%;
ilarity 66.7%;
Conservative 1
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28-DEC-2000; 2000US-00750395.
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 WPI; 2001-570626/64.
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Matches 4; Conser
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2 TFELSR 7
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7 AA;
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The sequence represents a schizophrenia-associated protein isoform (SPI). These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable in cerebrospinal fluid, serum or plasma and are useful markers of

Disclosure; Page 32; 148pp; English.

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The invention relates to a preparation comprising an isolated Bipolar

Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are

used to screen, diagnose or prognose of BAD or unipolar depression,

cetermine the stage or severity of BAD or unipolar depression, identify a

subject at risk of developing BAD or unipolar depression, or monitor the

ceffect of therapy in a subject. They are also used to screen for or

identify agents that interact with a DPI. These agents, antibodies

against the DPIs, and nucleic acids encoding the DPIs are used to treat

or prevent BAD or unipolar depression. Diseases that can be treated are

attention deficient disorder, a schizoaffective disorder, a bipolar or a

attention affective disorder. The DPIs are used in proteomics. The

proteomic approach of using DPIs for screening, diagnosis or prognosis of

BAD or unipolar depression overcomes the problems of using gene

expression analysis, such as not being able to obtain central nervous

system (CNS) tissue from a living patient under normal circumstances. The

present sequence is a DIP decreased in the CSF (cerebro-spinal fluid) of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
              schizophrenia, screening, prognosis, monitoring the results of therapy, identifying patients most likely to respond to a particular therapy and identification of new targets for drug treatment. SPI DNA is useful as anucleic acid probe to detect the presence of nucleic acids or SPIs
schizophrenia. The sequences can be used for treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Bipolar Affective Disorder; BAD; Depression-Associated feature; DF; Depression-Associated protein isoform; DFI; Cerebro-spinal fluid; CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic; attention deficient disorder; schizoaffective disorder; unipolar affective disorder.
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preparation for diagnosing or treating bipolar affected disorder unipolar depression, or for screening for modulators, comprises a associated protein isoform.
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                                                                                                                                                                                          1; Indels
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                                                                                                                                                Score 19; DB 4; I
Pred. No. 1.4e+06;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                      AAU26249 standard; peptide; 7 AA
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08-DEC-2000; 2000GB-00030050.
12-DEC-2000; 2000US-0254830P.
                                                                                                                                                     61.3%;
66.7%;
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                                                                                                                                                                                            4; Conservative
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Best Local Similarity
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                                                                                                                Sequence 7 AA;
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AAU26249
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Sequence 7 AA;

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The invention relates to methods and compositions for screening, diagnosis and prognosis of Schizophrenia. The method involves detecting the presence of Schizophrenia (SCH) Associated Features (SF8) and SCH Associated Protein Isoforms (SPIS) in samples, e.g. by electrophoresis, immunoassay or hybridisation assay, for diagnosing and monitoring SCH, studying the effectiveness of treatments and for identifying potential therapeutic agents. The method is used for (1) screening or diagnosis of SCH and the relative abundance of at least I chosen feature correlates with the presence or absence of SCH; and (2) monitoring the effect of therapy administered to a subject with SCH and the relative abundance of at least I chosen feature which correlates with the severity of SCH. The expression and activity of the SCH; and related molecules (e.g. cerondary messengers) are studied to diagnose SCH, monitor the progress of the disorder and the effectiveness of treatment and as targets to identify and produce potential therapeutic agents for the treatment of SCH. The paucity of detectable neuralgic defects distinguishes consequently the identification and characterisation of many cases. Consequently the identification and characterisation of cellular and/or molecular causative defects and neuropathies are cellular and/or miproved treatment of neuropsychiatric disorders. Adults14-Adults762 represent the amino acid sequences of schizophrenia-associated isoforms used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing and monitoring Schizophrenia by detecting the presence of Schizophrenia Associated Features and Schizophrenia Associated Protein Isoforms in samples of cerebrospinal fluid.
                                                                                                                 Gaps
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                                                                          Score 19; DB 4; Length 7; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Schizophrenia-associated isoform peptide #198.
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                                                                                                                                                                                                                                                                                           AAU15313 standard; peptide; 7 AA.
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2000US-00750395
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                                                                        Query Match 61.3%;
Best Local Similarity 66.7%;
Matches 4; Conservative
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subjects having BAD
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                                                                                                                                                     TLKLSR 7
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TFELSR
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                                     Sequence 7 AA;
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28-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for Alzheimer's disease in a mammal, by making two-dimensional array of a feature whose relative abundance correlates with disease, and comparing with abundance of the feature in samples of healthy persons.
                                                                                                Gaps
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digest;
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Rohlff C, Silber BM, Stiger TR, Sunderland PT;
White F, Williams SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; neuroprotective; nootropic; gene therapy; vaccine; Alzheimer's disease; Alzheimer's Disease-Associated Feature; Alzheimer's Disease-Associated Protein Isoform; API; tryptic Expression Reference Protein Isoform; ERPI; proteolysis.
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                          Score 19; DB 4; Length 7; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human API-125 tryptic digest peptide #8.
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                                                                                                                                                                                                                                                                                                                                                                                        ABB52355 standard; peptide; 7 AA
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28-NOV-2000; 2000US-0253647P.
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Query Match
Best Local Similarity 66..
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(PFIZ ) PFIZER
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Townsend RR,
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ABB52355
ID ABB52
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AC ABB52
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The invention relates to a novel antibody comprising a variable heavy

(VH) domain, variable light (VL) domain, VH complementarity determining

region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
antibody immunospecifically binds to a respiratory syncytial virus (RsV)
antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
and immunostimulant activity. The polynucleotides of the invention may
have a use in a vaccine, and in gene therapy. The antibody is useful for
treating or ameliorating a RSV infection in a human. The antibody is also
useful for preventing, treating or ameliorating one or more symptoms
associated with RSV infection in a mammal, e.g. cystic fibrosis,
bronchopulmonary dysplasia, congenital heart disease, congenital
immunodeficiency or acquired immunodeficiency, or after a bone marrow
transplant. The sequence represents a complementary determining region
c peptide from a human RSV antibody of the invention
                                                                                                                                                                                                 Human, variable heavy domain; variable light domain; CDR; VH; VL; RSV; complementarity determining region; respiratory syncytial virus; virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine; immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant; bronchopulmonary dysplasia; congenital heart disease; congenital immunodeficiency; acquired immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody for treating respiratory syncytial virus (RSV) infection, comprises a variable heavy/light domain or complementarity determining regions 1 - 3 of variable light/heavy chains, that immunospecifically binds to RSV antigen.
                                                                                                                                                               Human RSV antibody VL CDR2 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 55; 298pp; English.
                                         ABP66489 standard; peptide; 7 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Young JF, Koenig S, Johnson LS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-2000; 2000US-00724396.
28-NOV-2000; 2000US-00724531.
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                                                                                                                       (first entry)
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                                                                                                                       04-DEC-2002
                                                                                ABP66489;
RESULT 15
ABP66489
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Query Match 61.3%; Score 19; DB 5; Length 7; Best Local Similarity 80.0%; Pred. No. 1.4e+06; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps

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Search completed: June 2, 2004, 18:57:51 Job time: 50 secs

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June 2, 2004, 18:59:52; Search time 37.5 Seconds (without alignments) 52.517 Million cell updates/sec
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                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                           1155919 segs, 281338677 residues
                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                            US-09-712-819D-13
                                                                                                                                    1 LTLKLSR 7
                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 7
                                                                                                               Title:
Perfect score:
                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                      Sequence:
                                                                                                                                                                                             Searched:
                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 164, App	Sequence 164, App	Sequence 164, App	Sequence 198, App	Sequence 7, Appli	Sequence 370, App	Sequence 135, App	Sequence 145, App	Sequence 145, App	Sequence 135, App	Sequence 105, App	Sequence 13, Appl	-	Sequence 460, App	. di
e e	US-09-996-288-164	US-09-996-265-164	US-10-461-863-164	US-09-791-378-198	US-09-998-909-7	US-09-826-290-370	US-09-996-288-135	US-09-791-393-145	US-09-791-389-145	US-09-996-265-135	US-10-601-100-105	US-10-044-034-13	US-10-461-863-135	US-10-264-309-460	US-09-897-107-24
DB :	თ	10	15	σ	σ	თ	σ	10	10	50	12	13	12	16	σ
Query Match Length DB	7	7	7	7	7	7	7	7	7	7	7	7	7	7	9
Ouery Match	64.5	64.5	64.5	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	58.1
Score	20	20	20	19	19	19	19	19	19	19	19	19	19	19	18
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9 US-09-989-789-19 9 US-09-989-789-19 9 US-09-989-789-3 9 US-09-989-789-3 9 US-09-989-789-3	US-09-796-84 US-09-844-50 US-09-996-28 US-09-996-28 US-09-996-28	10 US-09 10 US-09 10 US-09 10 US-09 10 US-09	10 US-09-996-265 10 US-09-996-265 10 US-09-989-994 10 US-09-989-994 10 US-09-989-994 10 US-09-989-994	14 US-10-084-826-43 14 US-10-234-026-6 14 US-10-234-026-6 15 US-10-461-863-35 15 US-10-461-863-96 15 US-10-461-863-96 15 US-10-461-863-131 9 US-09-996-288-121
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ALIGNMENTS

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### Sequence 164

### Sequence 166

### Sequence
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61.3%;
66.7%;
                         Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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CRGANISM: Homo sapiens
US-09-998-909-7
                                                                                                                              | :|||
2 TFELSR 7
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2 TFELSR 7
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US-09-826-290-370
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US-09-998-909-7
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 164, Application US/10461863
Publication No. US20040018200A1
GENERAL INFORMATION:
APPLICANT: Oliver, Cynthia
APPLICANT: Allan, Christian
APPLICANT: Allan, Christian
APPLICANT: Allan, Christian
APPLICANT: Allan, Christian
APPLICANT: Chang, Stephen
TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORMUL
FILE REFERENCE: 10271-071-999
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: 60/388,920
PRIOR APPLICATION NUMBER: 60/388,920
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 209
SOFTWARE: Patentin version 3.1
SEQ ID NO 164
LENGTH: 7
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi TITLE OF INVENTION: and Treatment FILE REFERENCE: 10271-048-999 CURRENT APPLICATION NUMBER: US/09/996,265 CURRENT FILING DATE: 2001-11-28 NUMBER OF SEQ ID NOS: 259 SOFTWARE: Patentin version 3.1 SEQ ID NO 164 LENGTH: 7
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Sequence 198, Application US/09791378

Patent No. US20020142303A1

GENERAL INFORMATION:

APPLICANT: Parekh, Rajesh

TITLE OF INVENTION: SCHIZOPHRENIA

FILE REFERENCE: 9195-061-999

CURRENT APPLICATION NUMBER: US/09/791,378

CURRENT FILING DATE: 2001-02-23

PRIOR APPLICATION NUMBER: 09/750,395

PRIOR FILING DATE: 2000-12-28

NUMBER OF SEQ ID NOS: 677

SOFTWARE: Patentin version 3.0

SEQ ID NO 198

LENGTH: 7
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Matches 4; Conservative
                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-996-265-164
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CORGANISM: Homo sapiens
US-10-461-863-164
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CRGANISM: Homo sapiens
US-09-791-378-198
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2 TMKLS 6
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APPLICANT: White, Frost Applicant: Applicant: White, Frost Applicant: White, Frost Applicant: Williams, Stephen A.

TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of TITLE OF INVENTION: Alzheimer's Disease

FURRENT APPLICATION NUMBER: US/09/826,290

CURRENT FILING DATE: 2001-04-30

PRIOR APPLICATION NUMBER: US 60/194,504

PRIOR FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 492

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 7

TYPE: PRT
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Patent No. US20020164664A1

GENERAL INFORMATION:

APPLICANT: Havaty, John

APPLICANT: Briggman, Joseph

TITLE OF INVENTION: Detection and Treatment of Prostate Cancer;
FILE REFERENCE: MTP-027

CURRENT APPLICATION NUMBER: US/09/998,909

CURRENT FILING DATE: 2001-11-30

PRIOR PPLICATION NUMBER: US 60/250,284

PRIOR FILING DATE: 2000-11-30

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.0
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j Sequence 370, Application US/09826290

j Patent No. US20020164668A1

j GENERAL INFORMATION:

j APPLICANT: Friedman, David L.

j APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

j APPLICANT: Kimmel, Lida H.

j APPLICANT: Parekh, Rajesh Bhikhu

j APPLICANT: Porter, David M.

j APPLICANT: Potter, David M.

j APPLICANT: Solber, B. Michael

j APPLICANT: Silber, B. Michael

j APPLICANT: Sunderland, P. Trey

j APPLICANT: Townsend, Robert Reid

j APPLICANT: Townsend, Robert Reid
                                                        1; Indels
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    Length 7;
Score 19; DB 9;
Pred. No. 1e+06;
1; Mismatches
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Sequence 145, Application US/09791389

Sequence 145, Application US/09791389

Publication No. US2003032773A1

GENERAL INFORMATION:

APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri

APPLICANT: Farekt, Rajesh Bhikhu

APPLICANT: Tyen, Kerry Louise

APPLICANT: Tyen, Kerry Louise

TITLE OF INVENTION: Proteins, Genes and Their Use for

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)

TITLE OF INVENTION: and Unipolar Depression

FILE REFERENCE: 2543-1-001 NZ

CURRENT APPLICATION NUMBER: US/09/791,389

CURRENT FILING DATE: 2001-02-23

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-12-08

PRIOR PILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 308

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 135, Application US/0996265
Sequence 135, Application US/0996265
Publication No. US20030091584A1
GENERAL INFORMATION:
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: and Treatment
FILE REPERENCE: 10271-048-999
CURRENT APPLICATION NUMBER: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTHE Patentin version 3.1
SEQ ID NO 135
LENGTH: 7
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Pred. No. 1e+06;
1; Mismatches 0
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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US-09-996-265-135
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US-09-791-389-145
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2 TFELSR 7
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Patent No. US20020177126A1

GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: And Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT APPLICATION NUMBER: US/09/996,288
SOFTWARE: PatentIn version 3.1
SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 135
LENGTH: 7
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                                                  Score 19; DB 9; Length 7; Pred. No. 1e+06; 1; Mismatches 1; Indels
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                                                   66.7%;
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80.0%;
                                                  Query Match
Best Local Similarity 66.7
Matches 4, Conservative
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Best Local Similarity 80.0
Matches 4; Conservative
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CAGANISM: Homo sapiens
US-09-996-288-135
; ORGANISM: homo sapien
US-09-826-290-370
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CORGANISM: homo sapien
US-09-791-393-145
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Best Local Similarity
Matches 4; Conserv
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2 TFELSR 7
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Sequence 135, Application US/10461863
Publication No. US20040018200A1
GENERAL INFORMATION:
APPLICANT: Oliver, Cynthia
APPLICANT: Chang, Stephen
TITLE OF INVENTION: STABILIZED ANTI-RESPIRATORY SYNCYTIAL VIRUS (RSV) ANTIBODY FORM
FILE REFERENCE: 10271-071-99
CURRENT APPLICATION NUMBER: US/10/461,863
CURRENT APPLICATION NUMBER: 60/388,920
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 209
SOFTWARE: Patentin version 3.1
SEQ ID NO 135
LENGTH: 7
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US-10-264-300-460

IS Squence 460, Application US/10264309

PUBLICATION No. US2004002294A1

SQUENCE AGO, Application US/10264309

PUBLICATION No. US2004002294A1

APPLICANT: PRIBDWAN, DAVID L.

APPLICANT: FRIEDWAN, DAVID L.

APPLICANT: RAMENT, LIDA H.

APPLICANT: RAMENT, LIDA H.

APPLICANT: ROHLFF, CHRISTIAN

APPLICANT: SOURSE, DAVID M.

APPLICANT: SOURSE, PETER J.

APPLICANT: SOURSE, POLLY D.

APPLICANT: STIGER, HIGHAEL

APPLICANT: STUGER, HIGHAEL

APPLICANT: STUGER, HIGHAEL

APPLICANT: STUGER, THEY

APPLICANT: STUGER, PETER J.

APPLICANT: STUGER, PETER J.

APPLICANT: WHITE, W. FROST

APPLICANT: WHITE, W. FROST

APPLICANT: WILLIAMS, STEPHEN A.

APPLICANT: WOMERN: W. FROST

APPLICANT: WOMERN: OF 1010 DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE

TITLE REFREENCE: 202-10-03

CURRENT FILING DATE: 202-10-03

FRICK APPLICATION NUMBER: 60/326,708

PRICK PETING DATE: 201-10-03

NUMBER OF SQ ID NOS: 491

SEQ ID NO 460

LENGTH: 7
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Best Local Similarity 66.7
Matches 4; Conservative
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; 'CRGANISM: Homo sapiens
US-10-264-309-460
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US-10-461-863-135
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2 TFELSR 7
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                                                                                          Sequence 105, Application US/10601100

Sequence 105, Application US/2040072261A1

GENERAL INFORMATION:

APPLICANT: INNOGENETICS N.V.

TITLE OF INVENTION: Method for the Diagnosis and Differential Diagnosis of TITLE OF INVENTION: Neurological Diseases

FILE REFERENCE: 11362.0038.NPUS01

CURRENT APPLICATION NUMBER: US/10/601,100

CURRENT APPLICATION NUMBER: EP 02447121.1

PRIOR FILING DATE: 2002-06-21

PRIOR FILING DATE: 2002-07-17

NUMBER OF SEQ ID NOS: 113

SOFTWARE: Patentin version 3.2

LENGTH: 7
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CTHER INFORMATION: Description of Artificial Sequence: Synthetic
CTHER INFORMATION: Peptides
US-10-044-034-13
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Sequence 13, Application US/10044034

Publication No. US20020169264A1

GENERAL INFORMATION:

APPLICANT: JACKSON, DAVID C.

APPLICANT: BROWN, LORENA E.

APPLICANT: BROWN, LORENA E.

APPLICANT: BROWN, LORENA E.

APPLICANT: BRANDT, EVELYN R.

APPLICANT: BRANDT, EVELYN R.

TITLE OF INVENTION: POLYMERS INCORPORTING PEPTIDES

FILE REFERENCE: FBRC:006

CURRENT APPLICATION NUMBER: US/10/044,034

CURRENT FILING DATE: 2002-01-11

PRIOR FILING DATE: 1997-02-11

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-601-100-105
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US-10-461-863-135
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Sequence 24, Application US/09897107
; Sequence 24, Application US/09897107
; Patent No. US20020137094A1
; GENERAL INFORMATION:
    APPLICANT: YAMAGISHI, Akihiko
    TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HAVING
    TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODIN
    TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENCODIN
    TITLE OF INVENTION NUMBER: US/09/897,107
    CURRENT APPLICATION NUMBER: JP2000-201920
    PRIOR FILING DATE: 2001-07-04
    PRIOR FILING DATE: 2001-05-31
    NUMBER OF SEQ ID NOS: 104
    SOFTWARE: Patentin version 3:1
    SEQ ID NO 24
    LENGTH: 6
    TYPE: PRT
    ORGANISM: Saccharomyces cerevisiae
    US-09-897-107-24
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Search completed: June 2, 2004, 19:08:55 Job time: 38.5 secs

1 LTLKLS 6 : |||| 1 MMLKLS 6

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